

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2005, 10:53:33 ; Search time 5243 Seconds

(without alignments)
4239.850 Million cell updates/sec

Title: US-10-828-332-7

Perfect score: 3107

Sequence: 1 MGVSSSLPTMTSGDRYP.....LETPALATKYVTVYTNHAI 584

Scoring table:

BLOSUM62
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-DB=EST -QFMT=fstap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q= /cpn2 1 /uspt0 spool /US10828332/runat 17062005 170038 7263 /app query.fasta_1.775
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	2348	75.6	3675	3 AK038395	AK038395 Mus muscu
2	2348	75.6	3693	3 BC051384	BC051384 Mus muscu
3	2298	74.0	2671	9 AY406143	AY406143 Homo sapi
4	2280.5	73.4	2667	9 AY406145	AY406145 Mus muscu
5	2229.5	71.8	2671	9 AY406144	AY406144 Pan trogl
6	2219	71.4	2671	9 AY406144	AY406144 Pan trogl
7	2214	71.3	2748	9 AY401210	AY401210 Mus muscu
8	2156.5	69.4	4209	3 AK053447	AK053447 Mus muscu
9	2140	68.9	2611	9 AY401209	AY401209 Pan trogl

10	2025	65.2	3399	3 BC034118	BC034118 Mus muscu
11	1298.5	41.8	1484	3 CR717163	CR717163 Tetraodon
12	1294	41.6	782	6 CD353576	CD353576 UI-M-GMO-
13	1169	37.6	1051	9 CN504790	AL306790 Tetraodon
14	1151	37.0	711	7 CN409312	CN409312 170004243
15	1114.5	35.9	3879	3 AK032422	AK032422 Mus muscu
16	1066	34.3	653	1 AU296039	AU296039 AU296039
17	1034.5	33.3	973	4 B1827857	B1827857 603074065
18	1023	32.9	795	7 CN460548	CN460548 UI-M-HBO-
19	1019	32.8	678	5 BU205182	BU205182 604156686
20	1013	32.6	702	7 CK134839	CK134839 SB0204082
21	983	31.6	787	4 B1732193	B1732193 603352796
22	964	31.0	582	5 BP359939	BP359939 BP359939
23	952	30.6	608	4 BM490671	BM490671 P9P2n.pk0
24	943	30.4	679	5 BM964289	BM964289 UI-M-EQO-
25	928	29.9	732	6 CD609655	CD609655 56040124H
26	916.5	29.5	723	6 CA344834	CA344834 675311 NC
27	915.5	29.5	839	9 CNS028BY	AL185767 Tetraodon
28	885.5	28.5	1101	9 CNS04XAU	AL311439 Tetraodon
29	884.5	28.5	2182	3 AK034263	AK034263 Mus muscu
30	872.5	28.1	772	5 BX873944	BX873944 BX873944
31	860	27.7	666	9 CE724887	CE724887 tigr-g88-
32	821.5	26.4	645	6 BG261524	BG261524 602373277
33	817.5	26.3	895	4 BG261524	CD280064 G4469.19
34	800.5	25.8	665	6 CA408051	CA408051 STR00549
35	799	25.7	777	5 BU456417	BU456417 603217533
36	770.5	24.8	633	6 CB517356	CB517356 seaalrbs53
37	766.5	24.7	1029	9 CNS02AUZ	AL189044 Tetraodon
38	763.5	24.6	1736	3 AK002958	AK002958 Mus muscu
39	758	24.4	1078	9 CDS054KQ	AL320867 Tetraodon
40	752	24.2	754	6 CD609656	CD609656 56040124J
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42	735.5	23.7	872	9 CNS02JYJ	AL200851 Tetraodon
43	729	23.5	1148	8 CC208336	CC208336 CD261-44D
44	723	23.3	562	6 CD252943	CD252943 AGENCOURT
45	721	23.2	521	7 CN468842	CN468842 hh_Ab_Bra

ALIGNMENTS

RESULT 1	AK038395	3675 bp	linear	HTC 03-APR-2004
LOCUS	Mus musculus adult male hypothalamus cDNA, RIKEN full-length			
DEFINITION	enriched library, clone:A23002004 product:METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR, full insert sequence.			
ACCESSION	AK038395			
VERSION	AK038395.1	GI:26086504		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wachihi, M.,			

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--394-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium

5	2	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
AUTHORS		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL		Nature 420, 563-573 (2002)
REFERENCE	6	(bases 1 to 3675)

TITLE
JOURNAL
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayaishizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

FEATURES
SOURCE

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misc feature

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ORIGIN

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Best Local Similarity:	72.59%
Query Match:	75.57%
DB:	3
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Matches:	437
Conservative:	61
Mismatches:	83
Indels:	21
Gaps:	3

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Qy 222 TyrrGlnValAspArgTyrrCysLysThrCysProTyrrAspMetArgProThrGluAsn 241
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Qy 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrrAlaAla 341
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DEFINITION Homo sapiens GRM8 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY406143
VERSION AY406143.1 GI:39762117
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2671)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2671)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

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ORIGIN

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 Best Local Similarity: 75.44% Mismatches: 83
 Query Match: 73.96% Indels: 4
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US-10-828-332-7 (1-584) x AY406143 (1-2671)

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 AY406145
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AY406145 2667 bp DNA linear GSS 15-DEC-2003

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 DB 2230 GATCTCTACATCTTGTCTCACTTGGATACAGTATCTCTTGTATGCTCATTGTACTGTT 2289
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DEFINITION Mus musculus GRM8 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY406145
VERSION AY406145.1 GI:39762119
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2667)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2667)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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source
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342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES

Location/Qualifiers
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CDS

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ORIGIN

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US-10-828-332-7 (1-584) x AK053447 (1-4209)

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 LOCUS
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ACCESSION BC034118.1 GI:21706621

VERSION HTC.

KEYWORDS Mus musculus

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3399)

REFERENCE Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Caaviani, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Amberson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shchenko, Y.,
 Bouford, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalka, U., Smalil, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 3399)

Strausberg, R.

Direct Submission

Submitted (02-JUL-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 44 Row: 1 Column: 22

This clone was selected for full length sequencing because it

passed the following selection criteria: Hexamer frequency ORF

analysis

This clone has the following problem: frame shifted.

Location/Qualifiers

1. 3399

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/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

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Query Match: 65.18% Indels: 4

DB: 3 Gaps: 2

US-10-828-332-7 (1-584) x BC034118 (1-3399)

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Db 122 GGGCCATCACCATCTTTCGCAAAAGGGCTTCAATCGACGGATTTGACCAATACTTATG 181

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Qy	519	PheHisProGluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAla	538
Db	1682	TTCCATCCAGAGAGAACGTCGACAGACGGAGCGCCCTCAAGAGACCTCCACGATG	1741
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Db	1742	GCG 1744	
RESULT 11			
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DEFINITION	Tetraodon nigroviridis full-length cDNA.		
ACCESSION	CR717163		
VERSION	CR717163.1 GI:51215408		
KEYWORDS	HTC; cDNA; full-length; Tetraodon nigroviridis.		
SOURCE	Tetraodon nigroviridis		
ORGANISM	Tetraodon nigroviridis		
REFERENCE	1 (bases 1 to 1484)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-AUG-2004) Genoscope - Centre National de Sequençage - 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE		
COMMENT	(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) The sequences are based on single pass reads. More information available at http://www.genoscope.cns.fr/tetraodon.		
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Qy      273  AlaThrLeuPheValValThrPheValArgTyrAsnAspThrProIleValLysAla 292
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LOCUS

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DEFINITION
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VERSION
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AUTHORS
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COMMENT
FEATURES
source

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EST.
CD353576.1 GI:31146077
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 782)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9pbbs@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5
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Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was size
selected according to mRNA size fraction, ligated with Ecor
I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

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AUTHORS Roset Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernet,A., Fzames,C., Wincker,P., Brottier,P., Quetier,P.,
Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roset Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,P.,
Saurin,W., Bernet,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
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10899143
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AUTHORS Direct Submission
TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
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COMMENT This sequence is a single read and was generated as part of a large
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genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3879)
ADACHI, J., Aizawa, K., Akimura, T., Atakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
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Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: June 21, 2005, 11:28:54 ; Search time 280 Seconds
(without alignments)
3412.806 Million cell updates/sec

Title: US-10-828-332-7

Perfect score: 3107

Sequence: 1 MGVSSSLPTRMTSGFDYF.....LETPALATKQTVYVTHNAI 584

Scoring table:

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	Ygapop 10.0	Ygapext 0.5
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=fascap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
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-USER=US10828332 @CGN 1.1.177 @runat.17062005.170039.7279 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued Patents NA:*
- 2: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/BACKFILES.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3050.5	98.2	2838	US-09-820-809-1	Sequence 1, Appl
2	3050.5	98.2	4095	PCT-US91-09422-18	Sequence 18, Appl
3	3004.5	95.7	2736	US-08-617-785-1	Sequence 1, Appl
4	3004.5	96.7	2736	US-09-817-464-1	Sequence 0, Appl
5	3004.5	96.7	3431	US-09-641-318-1	Sequence 1, Appl
6	3004.5	96.7	3431	US-09-641-318-3	Sequence 3, Appl
7	3004.5	96.7	3884	US-09-016-434-1074	Sequence 1074, Ap
8	3004.5	96.7	3884	US-09-820-809-14	Sequence 14, Appl
9	2720.5	87.6	2426	PCT-US91-09422-20	Sequence 20, Appl
10	2370	76.3	3321	US-08-855-146-1	Sequence 1, Appl
11	2370	76.3	3321	US-08-855-146-3	Sequence 3, Appl
12	2348	75.6	3833	US-08-823-110-2	Sequence 2, Appl

13	2348	75.6	3833	3	US-08-604-298-2	Sequence 2, Appl
14	2328	74.9	2724	3	US-08-823-110-5	Sequence 5, Appl
15	2328	74.9	2724	3	US-08-604-298-5	Sequence 5, Appl
16	2219	71.4	2745	3	US-08-617-785-11	Sequence 11, Appl
17	2219	71.4	2745	4	US-09-817-464-11	Sequence 11, Appl
18	2219	71.4	3021	4	US-09-016-434-1118	Sequence 1118, Ap
19	2210	71.1	2997	1	US-08-453-862-1	Sequence 1, Appl
20	2210	71.1	2997	2	US-08-452-734A-1	Sequence 1, Appl
21	2210	71.1	2997	3	US-08-176-401B-1	Sequence 1, Appl
22	2210	71.1	2997	5	PCT-US94-14989-1	Sequence 1, Appl
23	2191.5	70.5	2766	3	US-08-617-785-13	Sequence 13, Appl
24	2191.5	70.5	2766	4	US-09-817-464-13	Sequence 13, Appl
25	2191.5	70.5	3804	3	US-08-617-785-3	Sequence 3, Appl
26	2191.5	70.5	3804	4	US-09-817-464-3	Sequence 3, Appl
27	2052.5	66.1	2961	2	US-08-407-875-1	Sequence 1, Appl
28	2052.5	66.1	2961	3	US-09-277-858-1	Sequence 1, Appl
29	2040.5	65.7	2670	3	US-09-126-280-1	Sequence 1, Appl
30	2022	65.1	2635	3	US-09-126-280-3	Sequence 3, Appl
31	1865.5	60.0	1588	3	US-08-617-785-7	Sequence 7, Appl
32	1865.5	60.0	1588	4	US-09-817-464-7	Sequence 7, Appl
33	1172.5	37.7	2619	3	US-08-337-797A-1	Sequence 1, Appl
34	1172.5	37.7	2619	3	US-08-337-797A-3	Sequence 3, Appl
35	1172.5	37.7	2619	3	US-09-258-523-1	Sequence 1, Appl
36	1172.5	37.7	2619	3	US-09-258-523-3	Sequence 3, Appl
37	1155.5	37.2	2637	3	US-08-794-158-1	Sequence 3, Appl
38	1155.5	37.2	2637	3	US-08-794-158-3	Sequence 3, Appl
39	1155.5	37.2	3410	4	US-09-016-434-1080	Sequence 1080, Ap
40	1150.5	37.0	2621	4	US-09-016-434-1490	Sequence 1490, Ap
41	1148.5	37.0	3919	1	US-08-072-574-5	Sequence 5, Appl
42	1148.5	37.0	3919	1	US-08-486-270-5	Sequence 5, Appl
43	1148.5	37.0	3919	3	US-08-367-264-5	Sequence 5, Appl
44	1148.5	37.0	3919	3	US-09-153-757-5	Sequence 5, Appl
45	1148.5	37.0	3919	4	US-09-459-715-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-820-809-1
; Sequence 1, Application US/09820809
; Patent No. 6608176
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARI, NIRUPA
; APPLICANT: ROOPER, STEPHEN D.
; TITLE OF INVENTION: TTASTE RECEPTOR FOR UMAMI (MONOSODIUM GLUTAMATE) TASTE
; FILE REFERENCE: 70373/275576
; CURRENT APPLICATION NUMBER: US/09/820,809
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-820-809-1

Alignment Scores:					
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Score:			Matches:	575	
Percent Similarity:	98.97%		Conservative:	2	
Best Local Similarity:	98.63%		Mismatches:	5	
Query Match:	98.18%		Indels:	1	
DB:	4		Gaps:	1	

US-10-828-332-7 (1-584) x US-09-820-809-1 (1-2838)

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Qy	22	SerArgThrLeuAspAsnAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn	41

Db 252 AGCCGCGCTGGAGCAACAACAGCGCAACATCTGTTTGGCCGAGTTCTGGGAGCAAC 311
Qy 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
Db 312 TTCCATTGCAAGTTGAGCGCGCAGCGCTCAAGAGGGAAGCCACATCAAGAAGTGACCC 371
Qy 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGlnGlnGluGlyLysValGlnPheVal 81
Db 372 AACCGAGAGCGCATCGGGCAGGACTCGGCCCTATGAGCAGGAGGGAAGTGTCAGTTCTGTG 431
Qy 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
Db 432 ATTGACGCTGTGTAGCCATGGCCACCGCTGCAAGCCCATGACCGCTGTGTCT 491
Qy 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
Db 492 GCGCGGTAGGACTCTGCCCTCGCATGACCCCGTGGATGGCACCCAGCTGCTTAAGTAC 551
Qy 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
Db 552 ATCAGGAAGCTCACTTCTAGGCAATTGCGGGAAACCTGTAACTTCAATGAGAACGGA 611
Qy 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
Db 612 GACGACACGCGCGCTACGACATCTACCACTGACCACTGCGCAATGGCTCGCGCGAGTAC 671
Qy 162 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 181
Db 672 AAGTCATCGCTCGTGACAGACACCTGCACTCAGATAGAGCGGATGACGTGGCCA 731
Qy 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
Db 732 GGGAGTGCCAGAGCTGCGCGCTTCCATCTGCAGTCTGCCCTCGACCGCGGGAGCGGA 791
Qy 202 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 221
Db 792 AAGAAGACTGTGAAGGCGATGGCTTGTCTGCTGGCACTGGCGAGCCCTGACCGGGTACCAG 851
Qy 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
Db 852 TACCAAGTGGACCGCTACACCTGTAAGACCTGCGCCCTACGACATGCGCGCCACAGAAAC 911
Qy 242 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 261
Db 912 GGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGTGGCGCGTG 971
Qy 262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 281
Db 972 CTGCCCTCTTCTTGGCGGTGGGATCGCCGCCAGCGTGTTCGTGGTGGTCACGTTT 1031
Qy 282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
Db 1032 GTGGCTTACACGATACCCCATCGTCAAGCCCTCGGGCGGGAGCTGAGCTAGTCTGTG 1091
Qy 302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
Db 1092 CTGGCGGCGCATCTTCTGTGTGTAGCCCATCTTCTTCATGATCGAGAGCCGAGCCTG 1151
Qy 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
Db 1152 GGGACCTGTTCCTCGCGCGATCTTCTAGGCTCGGCATGAGCATCAGCTACGCGGCC 1211
Qy 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
Db 1212 CTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGGCAACGCTCGTCAGT 1271
Qy 362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
Db 1272 GCGCGCGGTTCATCAGCGCGGCTCGCAGGTGGCCATCCTTCATCCTCATCTCCCTG 1331
Qy 382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401

Db 1332 CAGCTGCTCGGCATCTCGGTGTGGTTCGTGGTGAGACCCCTCCCACTCGTGGTGGACTTC 1391
Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
Db 1392 CAGGACCAAGCGGACACTTGACCCCGCTTTGCCAGGGGCGTGTCTCAAGTGGACATCTCG 1451
Qy 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
Db 1452 GACCTGTCCCTCATCTGCTGCTGGGCTACAGCATGCTGCTGATGGTCACGTGTACTGTG 1511
Qy 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
Db 1512 TAGCCCATCAAGACCCCGAGGCGTGCCTGAGACCTTCAACGAGGCCAAGCCCATCGGCTTC 1571
Qy 462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 481
Db 1572 ACCATGTACACCACTGCTGCTGTGGCTGGCTTTCATCCCATCTTTTGGCACCTCA 1631
Qy 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
Db 1632 CAGTCAGCCGACAAGCTGTATCATCCAGAACACCACTGACTGTCTCGTGAGTCTGAGC 1691
Qy 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521
Db 1692 GCTTCAGTGTCCCTGGGGATGCTCTACATGCCAAAGTCTACATCATCTCTCCACCG 1751
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
Db 1752 GAGCAGAACCTGCCAAGCGCAGCGAGTCTCAAGCCGTGGTTCACCGCGCCACCATG 1811
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 1812 TCCAAACAGTTTCACAGAGAGGCGACTTCAGGCCCAATGGGAGGACCAATCAGAGCTG 1871
Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrAsn 581
Db 1872 TGTGAGAACCTGGAGACCCAGCGCTGGCTACCAACAGACCTACGTACCTACCAAC 1931
Qy 582 HisAlaIle 584
Db 1932 CATGCCATC 1940

RESULT 2
PCT-US91-09422-18
; Sequence 18. Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481

; FILING DATE: 30-JAN-1991
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/626,806
 ; FILING DATE: 12-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 13952-6PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4095 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: SN30
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 463..3198
 PCT-US91-09422-18

Alignment Scores:
 Pred. No.: 0 Length: 4095
 Score: 3050.50 Matches: 583
 Percent Similarity: 91.67% Conservative: 0
 Best Local Similarity: 91.67% Mismatches: 1
 Query Match: 98.18% Indels: 53
 DB: 5 Gaps: 1

US-10-828-332-7 (1-584) x PCT-US91-09422-18 (1-4095)

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QY	14	-----	14
DB	1351	GCTCGCAGGGCCACACAGACCGGCACCTCTTTTGGATGGTTCGTATAGCTGGGGCTCC	1410
QY	14	-----	14
DB	1411	AAGAGTGCCCTGTGCTGGCCTTGAGGAGTGGCGGCGCAGTCACCATTCCTCCCC	1470
QY	15	-----GlyPheAspArgTyrPheSerSerArgThrLeuAspAsn	28
DB	1471	AAGAGGATGCTGTGTCGAGGGTTCGACCGCATCTCTCCAGCGCCAGCTGGACCAAC	1530
QY	29	ArgAspAsnIleTTPheAlaGluPheTTPGluAspAsnPheHisCysLysLeuSerArg	48
DB	1531	AGCGCGACATCTGGTTGCCAGTTCCTGGAGGACCACTTCATTTGCAAGTTGAGCCGC	1590
QY	49	HisAlaLeuLysGlySerHisIleLysCysThrAsnArgGluArgIleGlyGln	68
DB	1591	CACGCGCTCAAGAGGAGGACACATCAAGAAAGTGCCACCAACGAGAGCGCATCGGGCAG	1650
QY	59	AspSerAlaTyrGluGlnGluLysValGlnPheValIleAspAlaValTyrAlaMet	88
DB	1651	GACTCGGCTATGAGCAGGAGGAGGAGGTGCAGTTTCGTGATTGACGCTGTGTACGCCATG	1710
QY	89	GlyHisAlaLeuHisAlaMetHisArgAspLeuCysProGlyArgValGlyLysCysPro	108
DB	1711	GGCCAGCGCTGACGCCATGACCGCTGACCTGTGTCCCGCGCGGTAGGACTCTGCCCT	1770
QY	109	ArgMetAspProValAspGlyThrGlnLeuLeuLysTyrIleArgAsnValAsnPheSer	128
DB	1771	CGCATGGACCCGCTGGATGGCAGCCAGCTGCTTAAGTACATCAGGAACGTCAACTTCA	1830
QY	129	GlyIleAlaGlyAsnProValThrPheAsnGluAsnGlyAspAlaProGlyArgTyrAsp	148
DB	1830	-----	148
DB	1831	GGCATTGGGGGAACCTGTAACTTCAATGAGAACGACGACCGGGGGCTACGAC	1890
QY	149	IleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyrLysValIleGlySerTyrThr	168
DB	1891	ATCTACCAAGTACCAACTGGCTCGGCGGAGTCAAGGTTCATCGCTCGTGGACA	1950
QY	169	AspHisLeuHisLeuArgIleGluArgMetGlnTyrProGlySerGlyGlnGlnPro	188
DB	1951	GACCACCTGCACCTCAGAAATAGCGGATGCGCCAGGAGTGGCCAGCAGCTGCCG	2010
QY	189	ArgSerIleCysSerLeuProCysGlnProGlyGluArgLysLysThrValLysGlyMet	208
DB	2011	CGCTCATCTGCAGTCTGCCCTGCCAGCCCGGGGAGCGAAGAGACTGTGAAGGCATG	2070
QY	209	AlaCysCysTTPHisCysGluProCysThrGlyTyrGlnTyrGlnValAspArgTyrThr	228
DB	2071	GCTTGCTGCTGGCACTGGAGCCCTGACCGGGTACCAAGTGGACCGCTACACC	2130
QY	229	CysLysThrCysProTyrAspMetArgProThrGluAsnArgThrSerCysGlnProIle	248
DB	2131	TGTAAGACCTGCCCTTACGACATGCGGCCCAACAGAAACCGCAGGCTGCCAGGCCATC	2190
QY	249	ProIleValLysLeuGluTyrAspSerProTTPAlaValLeuProLeuPheLeuAlaVal	268
DB	2191	CCCATCGTCAAGTTGGAGTGGACTCGCGCGGGCGGTGCTGCCCTCTTCTCGCCGCTG	2250
QY	269	ValGlyIleAlaAlaThrLeuPheValValThrPheValArgTyrAsnAspThrPro	288
DB	2251	GTGGCATCGCGCCACGCTGTTCTGTTGGTGTTCACGTTTGTGGCTACACGATACCCCC	2310
QY	289	IleValLysAlaSerGlyArgGluLeuSerTyrValLeuLeuAlaGlyIlePheLeuCys	308
DB	2311	ATCGTCAAGGCTCGCGCGGAGCTGAGTACGTGCTGTGGCGGGCATCTTCTGTGCTC	2370
QY	309	TyrAlaThrThrPheLeuMetIleAlaGluProAspLeuGlyThrCysSerLeuArgArg	328
DB	2371	TACGCCACTACTCTCTCATGATCGCAGCGCGGACCTGGGACCTGTTGGCTCGCCGC	2430
QY	329	IlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAlaLeuLeuThrLysThrAsnArg	348
DB	2431	ATCTCTTAGGGCTCGGCATGAGCATCAGTACGCGGCGCTGCTGACCAAGACCAACGC	2490
QY	349	IleTyrArgIlePheGluGlnGlyArgSerValSerAlaProArgPheIleSerPro	368
DB	2491	ATTTACCGCATCTTTGAGCAGGCGCAACGGTCGGTCAGTGGCCCGCTTTCACGCCCG	2550
QY	369	AlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeuGlnLeuLeuGlyIleCysVal	388
DB	2551	GCCTCGAGCTGGCCATCACCTTCATCTCATCTCCCTGACAGCTGCTCGGCATCTGCGTG	2610
QY	389	TrpPheValValAspProSerHisSerValValAspPheGlnAspGlnArgThrLeuAsp	408
DB	2611	TGGTTCTGGTGGACCCCTCCACCTCGGTGGTGGACTTCCAGGACCAACGAGACATTGAC	2670
QY	409	ProArgPheAlaArgGlyValLeuLysCysAspIleSerAspLeuSerLeuIleCysLeu	428
DB	2671	CCCCCTTTGGCAGGCGGTGCTCAAGTGGCAGCATCTCGGACCTGCTCCCTCATCTGCTG	2730
QY	429	LeuGlyTyrSerMetLeuLeuMetValThrCysThrValTyrAlaIleLysThrArgGly	448
DB	2731	CTGGCTACAGCATGCTGCTGATGGTCAGGTGCTGCTGATGAGCTTCAAGACCCGAGGC	2790
QY	449	ValProGluThrPheAsnGluAlaLysProIleGlyPheThrMetTyrThrThrCysIle	468
DB	2791	GTGCCGAGACCTTCAACGAGGCCAAGCCCATCGGCTTCCACCATGTACACCACTGCATT	2850
QY	469	ValTrpLeuAlaPheIleProIlePhePheGlyThrSerGlnSerAlaAspLysLeuTyr	488
DB	2851	GTCTGGCTGGCTTTCATCCCATCTTTTGGACCTCACAGTCAAGCGGACCAAGCTGTAC	2910
QY	489	IleGlnThrThrThrThrValSerValSerLeuSerAlaSerValSerLeuGlyMet	508
DB	2911	ATCCAGAACACCACTACGCTCTCCGAGTCTGAGCGCTTTCAGTGTCTCTCGGGGATG	2970

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Qy 509 LeuTyrMetProLysValTyrIleLeuPheHisProGluGlnAsnValProLysArg 528
Db 2971 CTCTACATGCCCAAGATCTACATCTCTTCACCCGGAGCAGAACGTGCCCAAGGC 3030
Qy 529 LysArgSerLeuLysAlaValValThrAlaAlaThrMetSerAsnLysPheThrGlnLys 548
Db 3031 AAGCGCAGTCTCAAAAGCGGTGTCCCGCCGCCACCATGTCCCAACAAAGTTCACACAGAAG 3090
Qy 549 GlyAsnPheArgProAsnGlyGluAlaLysSerGluLeuCysGluAsnLeuGluThrPro 568
Db 3091 GGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTGTGTGAGAACCTGGAGACCCCA 3150
Qy 569 AlaLeuAlaThrLysGlnThrTyrValThrThrAsnHisAlaIle 584
Db 3151 CGCTGGCTACCAACAGACCTACGTACCTACACCAACCATGCCATC 3198

RESULT 3
US-08-617-785-1
; Sequence 1, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 1
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2736)
US-08-617-785-1

Alignment Scores:
Pred. No.: 0 Length: 2736
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 3 Gaps: 1

US-10-828-332-7 (1-584) x US-08-617-785-1 (1-2736)
Qy 3 GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 988 GGTGCTGTACGATCCTCCCAAGAGGATGTCGATACGAGGCTTCGACCGCTACTTCTCC 1047
Qy 22 SerArgThrLeuAspAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 41
Db 1048 AGCGGCACGTGGACCAACACCGCGCAACATCTGGTTTGGCGAGTTCTGGGAGGACAAAC 1107
Qy 42 PheHisCysLysLeuSerArgHisAlaLeuLysGlySerHisIleLysLysCysThr 61
Db 1108 TTCCACTGCAAGCTGAGCGCCCTCAAGAGGAGGCGACCGCTCAAGAGTGCAC 1167
Qy 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 81
Db 1167
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Db 1168 AACCGTGAGCGAAATTGGCAGGATTACGCTTATGACGAGGAGGGGAAAGGTGCTGTTGTG 1227
Qy 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
Db 1228 ATCGATCCGTGTACGCGCATGGGCCACGCGTGCACGCCATGCACCGTGACCTGTGTGTC 1287
Qy 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
Db 1288 GCGCGCTGGGGCTCTGCCCGCGCATGACCCCTGTAGATGGCACCCAGCTGCTTAAGTAC 1347
Qy 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
Db 1348 ATCCGAAACGTCACCTTCTCAGGCATCGCAGGAAACCTCTGACCTTCAATGAGATGGA 1407
Qy 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
Db 1408 GATGCGCTGGGGCTGTATGACATCTACCAATACAGCTGCGCAACAGATTCCTGCGGAGTAC 1467
Qy 162 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 181
Db 1468 AAGGTCACTGGCTCCTGGACTGACCACTGCACCTTAGAATAGACGCGATGCACCTGGCG 1527
Qy 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
Db 1528 GGGAGCGGCGCAGCAGCTGCCCGCTCCATCTGCAGCCTGCCCTGCCAACCGGGTGAGCGG 1587
Qy 202 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 221
Db 1588 AAGAAGACAGTGAAGGCGATGCTTGTCTGCGCACCTGCGAGCCTTGACACAGGATCCAG 1647
Qy 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
Db 1648 TACCAAGTGGACCGCTACACCTGTAAAGCGTGCTCTATGACATGCGGCCACACAGAGAAC 1707
Qy 242 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 261
Db 1708 CGCACGGGCTGCCGGCCATCCCATCATCAAGCTTGAGTGGGGCTGCCCTGGGGCGGTG 1767
Qy 262 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValValThrPhe 281
Db 1768 CTGCCCCCTCTTCTTGGCCGTGGTGGCATCGCTCCACGTTGTTCTGGTGATCACCTTT 1827
Qy 282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
Db 1828 GTGGCTACAAACGACACGCCCATCGTCAAGSCCTCGGGCGTGAACCTAGCTAGCTGCTG 1887
Qy 302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
Db 1888 CTGGCAGGCATCTTCTGTGTGTATGCCACCATCTTCCTCATGATCGCTGAGCCGACCTT 1947
Qy 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
Db 1948 GGCACCTGCTGCTGCGCCGAAATCTTCTGGGACTAGGGATGACATCAGCTATGACGCC 2007
Qy 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
Db 2008 CTGCTACCAAGACCAACCGCATCTACCGCATCTTCGAGCAGGCGCAAGCGCTCGTCA 2067
Qy 362 AlaProArgPheLeuSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
Db 2068 GCGCCAGCTTCATCAGCCCGCTTCACAGCTGGCCATCACCTTTCAGCCTCATCTCGGTG 2127
Qy 382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401
Db 2128 CAGTGTGTGGCATCTGTGTGTGGTTGTGTGGACCCCTCCCACTCGGTGGTGACCTTC 2187
Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
Db 2188 CAGGACCGGCGACACTCGACCCCGCTTCGCCAGGGGTGTGCTCAAGTGTGACATCTCG 2247
Qy 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
Db 2248 GACCTGTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2307
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QY 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaIysProIleGlyPhe 461
 DB 2308 TATGCCATCAAGACACGCGCGTGGCCGAGACCTTCAATGAGGCCAAGCCCATTTGGCTTC 2367
 QY 462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 481
 DB 2368 ACCATGTACACCACTTGCATCGTCTGGCTGGCTTCATCCCATCTTTTGGCACCCTG 2427
 QY 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 501
 DB 2428 CAGTCGGCGGACAAAGCTGTACATCCAGACGACGCTGACGCTCTCGTGAGTCTGAGC 2487
 QY 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro 521
 DB 2488 GCCTCGGTGCTCCCTGGGAATGCTTACATGCCCAAGTCTACATCATCTCTTCCACCG 2547
 QY 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
 DB 2548 GAGCGAAGCTGCCACGCGGAGCGGAGCTTCAAGCGCTGTACGGCGGCCACCATG 2607
 QY 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
 DB 2608 TCCAAACAGTTTCAACGAGAGGCAACTTCGGGCCCAACGAGAGGCGCAAGTCTGAGCTC 2667
 QY 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 581
 DB 2668 TCCGAGAACCTTGGCGCCCGAGCGCTGGCCACCAACAGACTTACGTCACTTACACCAAC 2727
 QY 582 HisAlaIle 584
 DB 2728 CATGCAATC 2736

RESULT 4

US-09-817-464-1
 ; Sequence 0, Application US/09817464
 ; Patent No. 6515107
 ; GENERAL INFORMATION:
 ; APPLICANT: Flor, Peter J.
 ; APPLICANT: Kuhn, Ranier
 ; APPLICANT: Lindaur, Kristen
 ; APPLICANT: Puttner, Irene
 ; APPLICANT: Knopfel, Thomas
 ; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
 ; FILE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
 ; FILE REFERENCE: 4-19679/A/PCT
 ; CURRENT APPLICATION NUMBER: US/09/817,464
 ; EARLIER FILING DATE: 2001-03-26
 ; EARLIER APPLICATION NUMBER: US/08/617,785
 ; EARLIER FILING DATE: 1996-03-19
 ; EARLIER APPLICATION NUMBER: EPO 9416553.7
 ; EARLIER FILING DATE: 1994-08-19
 ; EARLIER APPLICATION NUMBER: EPO 93810663.0
 ; EARLIER FILING DATE: 1993-09-20
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO SEQ ID NO 1
 ; LENGTH: 2736
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(2736)
 US-09-817-464-1

Alignment Scores:

Pred. No.: 0 Length: 2736
 Score: 3004.50 Matches: 564
 Percent Similarity: 97.77% Conservative: 6
 Best Local Similarity: 96.74% Mismatches: 12
 Query Match: 96.70% Indels: 1
 DB: 4 Gaps: 1

US-10-828-332-7 (1-584) x US-09-817-464-1 (1-2736)

QY 3 GlyValSerSerSerLeuProThrArgMetThr----SerGlyPheAspArgTyrPheSer 21
 DB 988 GGTGCTGTACAGATCTCTCCCAAGAGGATGTCGTCACGAGGCTTCGACCGCTACTCTCC 1047
 QY 22 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 41
 DB 1048 AGCCGACCGCTGGACCAACACCGCGCGCAACATCTGGTTTGGCGAGTTCTGGGAGGACAA 1107
 QY 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
 DB 1108 TTCCACTGCAAGCTGAGCGCGCACGCCCTCAAGAAGGCGCAGCAGCTCAAGAAGTGACCC 1167
 QY 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 81
 DB 1168 AACCGTGAGCGAATTTGGCGAGATTTCAGCTTATGAGCAGGAGGAGGAGGAGTTCAGTTG 1227
 QY 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
 DB 1228 ATCGATGCGGTGTACGCCATGGCGCACCGCTGCACGCCATGCACCGTGTGTGCC 1287
 QY 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
 DB 1288 GCGCGGTGGGGCTCTGCGCGCATGACCTGTAGATGGCACCACCGCTGCTTAAGTAC 1347
 QY 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
 DB 1348 ATCCGNAACGTCACTTCTCAGGCATCGCAGGAACCTGTGACCTTCAATGAGAATGGA 1407
 QY 142 AspAlaProGlyArgTyrAspIleTyrGlnLeuArgAsnGlySerAlaGluTyr 161
 DB 1408 GATCGCGCTGGCGCTATGACATCTACCAATACCAAGCTGCGCAACGATTTCTGCCGAGTAC 1467
 QY 162 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 181
 DB 1468 AAGGTCAITGGCTCTCGGACGTGACCACTGACCTTAGAATAGACGAGATGACCTGGCG 1527
 QY 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
 DB 1528 GGGAGCGGACGAGCTGCCCGCTCCATCTGACGCTGCCCAACCGGGTGGCGG 1587
 QY 202 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 221
 DB 1588 AAGAAGACAGTGAAGGCGCATGCTTGTCTGTGCGACCTGCGAGCTTGACAGGGTACCAG 1647
 QY 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
 DB 1648 TACCAGGTGGACCGCTACCTGTAAAGACGTGTCCTATGACATCGGCGCCACAGAGAAC 1707
 QY 242 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 261
 DB 1708 CGCAGCGGCTGCCGCGCCATCCCATCATCAAGCTTGAGTGGGGCTGCCCTGGGCGGTG 1767
 QY 262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 281
 DB 1768 CTGCCCCCTCTTCTGCGCGGTGGCATCGCTGCCACGTTGTGCTGTGTATCATACCTTT 1827
 QY 282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
 DB 1828 GTGCGCTACACAGACGCCCATCTCAAGGCCCTCGGGCCCTGGAAGTGAAGTGAAGTGA 1887
 QY 302 LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 321
 DB 1888 CTGGCAGGCATCTTCTGCTGTATGCCACCACTTCTCATGATCGCTGAGCCGACCTT 1947
 QY 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
 DB 1948 GGCACCTGCTCGCTGCGCGGAATCTTCTGCGGACTTAGGGAATGAGCATCAGCTATGACGC 2007
 QY 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
 DB 2008 CTGCTCACCAGACCAACCGCATCTACCGCATCTTCGAGCAGGGGCAAGCGCTCGCTCAGT 2067

Qy 362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
Db 2068 GCGCCAGCTTCATCAGCCCGCCCTCAGAGTGGCCATCACCTTCAGCCTCATCTCGCTG 2127
Qy 382 GlnLeuLeuGlyIleCysValTrrPheValValAspProSerHisSerValValAspPhe 401
Db 2128 CAGCTGCTGGGCATCTGT 2187
Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLeuCysAspIleSer 421
Db 2188 CAGGACGAGCGACATCGACCCCGCTTCGCCAGGGGTGTGTCAAGTGTGACATCTCG 2247
Qy 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
Db 2248 GACCTGTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2307
Qy 442 TyrAlaIleIleThrArgGlyValProGluThrPheAsnGluAlaIleProIleGlyPhe 461
Db 2308 TATGCCATCAAGACACACGCGGCTGCCGAGACCTTCAATGAGGCCAAGCCATTGGCTTC 2367
Qy 462 ThrMetTyrThrThrCysIleValTrrPheIlePheIleProIlePheGlyThrSer 481
Db 2368 ACCATGTACACCACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2427
Qy 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
Db 2428 CAGTCGCGCGCAAGCTGTATCATCAGACGACGACGCTGCTGCTGCTGCTGCTGCTGCTG 2487
Qy 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTrrIleIleLeuPheHisPro 521
Db 2488 GCCTCGGTGCTCCCTGGGAATGCTCTACATGCCAAAGTCTACATCATCTCTTCCACCG 2547
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 541
Db 2548 GAGCAGACAGCTGCCAAGCGAAGCGACGCTCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 2607
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 2608 TCCAAACAGTTTACGCGAAGGGCACTTCGCGCCCAACGAGAGGCGCAAGTCTGAGCTC 2667
Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 581
Db 2668 TGCAGAACCTTGAGCGCCCGACGCTGCGCCACCAACAGACTTACGTCACTTACACCAAC 2727
Qy 582 HisAlaIle 584
Db 2728 CATGCAATC 2736

RESULT 5

US-09-641-318-1
; Sequence 1, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; WU, SU
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELI LILLY AND COMPANY
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: INDIANA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,318

FILING DATE: 18-Aug-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/816,178A
FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: GAYLO, PAUL J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10579
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3431 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 26..2761
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-641-318-1

Alignment Scores:
Pred. No.: 0 Length: 3431
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 3 Gaps: 1

US-10-828-332-7 (1-584) x US-09-641-318-1 (1-3431)

Qy 3 GlyValSerSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 1013 GGTGCTGTCTACGATCTCTCCCAAGAGGATTCGCGTACGAGGCTTCGACCGCTACTTCTCC 1072
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Db 1673 TACCAAGTGGACCGCTACACCTGTATAGACGTGTCCCTATGACATGGCGCCACAGAGA 1732
QY 242 ArgThrSerCysGlnProIleValLysLeuGluTrpAspSerProIleAlaVal 261
Db 1733 CGCAGGGCTGCGGCGCCATCCCATCATCAAGCTTGAGTGGGCTCGCCCTGGGCGGTG 1792
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Db 1793 CTGCCCTCTTCTGCGCGTGGGCGATCGCTGCCACCTGTGCTGTGTGATCACTTT 1852
QY 282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
Db 1853 GTGGCTACACGACACGCGCCATCGTCAAGGCTCGGGCGGTGAACCTGAGCTACGTGCTG 1912
QY 302 LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 321
Db 1913 CTGGCAGGATCTTCTGTGCTATGCCACCATCTTCTCATGATCGCTGAGCGCGACTT 1972
QY 322 GlyThrCysSerLeuArgGlyPheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
Db 1973 GGCACCTGCTGCGCGCGCATCTTCTGCGGACTAGGATGAGCATCAGTATGCGAGCC 2032
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Db 2093 GCGCCACGGTTCATCAGCCCGGCTCAGAGCTGGCCATCAGCTTACGCTCATCTGCTG 2152
QY 382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401
Db 2153 CAGCTGCTGGGCATCTGTGTGTTGTGTGGAGCCCTCCCACTCCGCTGGTGGACTTC 2212
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QY 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
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Db 2393 ACCATGTACACCATCTGATCGCTGCTGGTGGCTTTCATCCCATCTTCTTTGGSCACTCG 2452
QY 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
Db 2453 CAGTGGCGCGCAAGCTGTACATCCAGACGACGCTGACCGTCTCGGTGAGTCTTGAGC 2512
QY 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521
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QY 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 2633 TCCAAACAGTTCCGCGAAGGGCAACTTTCGCGCCCAACGGAGAGGCCAAGTCTGAGCTC 2692

QY 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 581
Db 2693 TCGGAGAACCTTTGAGGCCCCAGCGCTGGCCACCAACAGACTTACGTCACTTTACACCAAC 2752
QY 582 HisAlaIle 584
Db 2753 CATGCAATC 2761
RESULT 6
US-09-641-318-3
; Sequence 3, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; WU, SU
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELI LILLY AND COMPANY
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: INDIANA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,318
; FILING DATE: 18-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,178A
; FILING DATE: 12-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: GAYLO, PAUL J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10579
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-641-318-3
Alignment Scores:
Pred. No.: 0 Length: 3431
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 3 Gaps: 1
US-10-828-332-7 (1-584) x US-09-641-318-3 (1-3431)
QY 3 GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 1013 GGUGUGUCAGUCCUCCUCCCAAGAGGAUGCCGUAACGAGGCUUCCGCGUACUUCUCC 1072
QY 22 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 41
Db 1073 AGCCGACGCGUGGACAAACACCGCGCAACAUUGGUUUGCCGAGUUCUGGAGGACAAAC 1132
QY 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleIleLysCysThr 61

Db 1133 UUCACUGCAAGCUGAGCGGCCACCGCCUCCUAGAAGGGCAGCCACGUCUACAAGAGUGGCACC 1192
Qy 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 81
Db 1193 AACCGUGAGCGAAUUGGCGAGAUUACGUUAGAGCAGGGAGGAGGUGGAGCGAUUUGUG 1252
Qy 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
Db 1253 AUCGAUGCCGUGUAGCGCCAUUGGGCCACCGCGUGCAUGCGCAGCGUGACCGUGUCC 1312
Qy 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
Db 1313 GCGCGUGGGGCGUCUGCGCGCGAUGACCGUGAUGGCGACCCAGCUGCUUAAGUAC 1372
Qy 122 IleArgAsnValAsnPheSerGlyTleAlaGlyAsnProValThrPheAsnGluAsnGly 141
Db 1373 AUCCGAAACGUCACUUCUCAGGCAUCGACGGGAACCCUGUGACCUUCAAUGAGAAUGGA 1432
Qy 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
Db 1433 GAUGCGCCUGGGCGUAGUACAUCUACCAUACAGCUGCGCAACGAUUCUGCGGAGUAC 1492
Qy 162 LysValIleGlySerTyrThrAspHisLeuHisLeuArgIleGluArgMetGlnTyrPro 181
Db 1493 AAGGUAUUGGCUCCUGGACUACCCACCGUACCUUAGAAUAGAGCGGAUGACUGGCG 1552
Qy 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
Db 1553 GGGAGCGGGCAGCAGCUGCGCCCGUCCAUUCUGACGCGCCUCCGCAACCGGGUGAGCG 1612
Qy 202 LysLysThrValLysGlyMetAlaCysCysTyrHisCysGluProCysThrGlyTyrGln 221
Db 1613 AAGAAGACAGUAGAGGGCAUGCCUUGCUGUGGCAUCUGCGAGCCUUGACAGGUGUCCAG 1672
Qy 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
Db 1673 UACGAGUGGACCGCUACACCUAGAACGUGUCCUUAUGACAUGCGGCCACAGAGAAC 1732
Qy 242 ArgThrSerCysGlnProIleProIleValLysLeuGluTyrAspSerProTyrAlaVal 261
Db 1733 CGCAGCGGCGCGCGCCCAUCCCAUACAAGCUUAGUGGGGCGUCGCCCGCGCGUG 1792
Qy 262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValValThrPhe 281
Db 1793 CUGCCCUUCCUGCGCGCGGCGCAUCGCGCACGUUGUUGUGGUAUACACCUU 1852
Qy 282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
Db 1853 GUGGCUACACGACACGCGCCUAGCUAAGCGCCUGCGGCGGUAACUAGACUAGUGUGUG 1912
Qy 302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
Db 1913 CUGGAGCAUCUUCUGUGUAGUAGCCACCCUUCUAGUAGUGCGUGAGCGCGACCUU 1972
Qy 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
Db 1973 GCACCGUCGCGCGCGCGGAAUUCUUGGGAUAGGGAUGAGCAUCAGCUAGCGAGCC 2032
Qy 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
Db 2033 CUGCUACCAAGACCAACCGCAUCUACCGCAUCUUCGAGCAGGGCAAGCGCGUGUGU 2092
Qy 362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
Db 2093 GCGCCACGCUUACGAGCGCGCCUACAGCUGGCAUCCUUCAGCCUUCAGCCUUCUGUG 2152
Qy 382 GlnLeuLeuGlyIleCysValTyrPheValValAspProSerHisSerValValAspPhe 401
Db 2153 CAGCUGCGGGAUCUUGUGUGUUGUUGUGGAGACCCUCCUCCACUUGGUGGAGCUUC 2212
Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
Db 2213 CAGGACGAGCGGACACUCGACCCCGCUUCGCGAGGGGUGUGCUAAGUGUGACUUCUG 2272

Qy 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
Db 2273 GACCUUGUGCUAUCUUGCGUGUGGCUACAGCAUGCUGCUAGUGUACGUGACCGUG 2332
Qy 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
Db 2333 UAUGCCAUAAGACACGCGCGUGCGCCAGAGACCUUCAAUGAGGCGCAAGCCCAUUGGCUUC 2392
Qy 462 ThrMetTyrThrThrCysIleValThrLeuAlaPheIleProIlePhePheGlyThrSer 481
Db 2393 ACCAUGUACACCAUUGCUGUGUGCGUGCCUUAUCCCAUUCUUCUUGGACCCUG 2452
Qy 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
Db 2453 CAGUGCGCCCAACAGCUGUACUCCAGACGACGACGCGUGCUGCGUGGAGUGUGAGC 2512
Qy 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuLeuPheHisPro 521
Db 2513 GCUCGUGUGUCCUGGGAUUGCUCUACUAGCCCAAGUCUACAUCAUCCUUCUCCACCG 2572
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 541
Db 2573 GAGCAGAACCGUGCCAAAGCGCAGCGCCUCAAAGCGGCUUACGGCGGCGCCACCAUG 2632
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 2633 UCCNAAAGUUCACGCAAGAGGGCAUUCUGGCGCCCAACGAGAGGCGCAAGUCUGAGCUC 2692
Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrAsn 581
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RESULT 7

US-09-016-434-1074
; Sequence 1074, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555


```
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARI, NIRUPA
; APPLICANT: ROBER, STEPHEN D.
; TITLE OF INVENTION: TASTE RECEPTOR FOR UMAMI (MONOSODIUM GLUTAMATE) TASTE
; FILE REFERENCE: 70373/275576
; CURRENT APPLICATION NUMBER: US/09/820,809
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,454
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 3884
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-820-809-14

Alignment Scores:
Pred. No.: 0 Length: 3884
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 4 Gaps: 1

US-10-828-332-7 (1-584) x US-09-820-809-14 (1-3884)
QY 3 GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
DB 1158 GGTGTGTACAGGATCTCTCCCAAGAGGATGTCGCTACGAGGCTTCGACCGCTACTTCTCC 1217
QY 22 SerArgThrLeuAspAsnArgAsnIleTTPheAlaGluPheTTPGluAspAsn 41
DB 1218 AGCGCAGCTGGACAAACCGCGCAACATCTGTGTTGCGAGTTCTGGAGGAGCAAC 1277
QY 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
DB 1278 TTCCACTGCAGCTGAGCGGCCACGCCCTCAAGAGGCGCAGCCAGTCAAGAGTGCACC 1337
QY 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 81
DB 1338 AACCGTAGCGAAATTTGGGAGGATTTACGTTTATGAGCAGGAGGGGAGAGTTCAGTTTGTG 1397
QY 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
DB 1398 ATCGATGCGGTGTAGCCATGCGCCACCGCTGACGCCATGACCGTGTGTCCTTAAAGTAC 1457
QY 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
DB 1458 GGCCCGTGGGGCTCTGCGCGGCATGGACCTGTAGATGGCACCCAGCTGCTTAAAGTAC 1517
QY 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
DB 1518 ATCCGAAACGTCAACTTCTCAGGCATCGCAGGAACCCCTGTGACCTTCAATGAGATGGA 1577
QY 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
DB 1578 GATGCGCTGGCGCGTATGACATCTACCAATACCAGCTGCGCAACGATTCGCGGAGTAC 1637
QY 162 LysValIleGlySerTyrThrAspHisLeuHisIleGluArgIleGluArgMetGlnTyrPro 181
DB 1638 AAGGTCAATGCTCTCTGAGCTGACCACTGCACCTTAGAATAGAGCGGATGCACTGGCCG 1697
QY 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
DB 1698 GGGAGCGGGCAGCAGCTGCCCGCTCCATCTGCAGCTGCGCTGCGCAACCGGGTGAGCGG 1757
QY 202 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 221
DB 1758 AAGAAGACAGTGAAGGGCATGCTGCTGCTGGCAGTTCGCGAGCTTCGACAGGGGTACCAG 1817
QY 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
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DB 1818 TACCAGGTGGACCGCTACACCTGTAAAGCGTGTCCCTATGACATGCGGCCCCACAGAGAAC 1877
QY 242 ArgThrSerCysGlnProIleProIleValIleuGluTyrPaspSerProTyrAlaVal 261
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QY 262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 281
DB 1938 CTGCCCCCTCTCTCTGGCGGTGGGCAATCGTGCACAGTTGTTCGTTGGTATCACCTTT 1997
QY 282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
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QY 302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
DB 2058 CTGGCAGGCATCTCTCTGTCTATGCCACCACTTCTCATGATCGCTGAGCGCCGACCTT 2117
QY 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
DB 2118 GGCACCTGCTCGCTGCGCGCCGAATCTTCTGGGACTAGGGATGAGCATCAGCTATGCAGCC 2177
QY 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
DB 2178 CTGCTCAACAAGACCAACCGCATCTACCGCATCTTCGAGCAGGCGCAAGCGCTCGTCAGT 2237
QY 362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuLeuSerLeu 381
DB 2238 GCGCCACGCTTCATCAGCGCGCGCTCACAGTGGCCATCACCTTTCAGCCTCATCTCGGTG 2297
QY 382 GlnLeuLeuGlyIleCysValTyrPheValValAspProSerHisSerValValAspPhe 401
DB 2298 CAGCTGTGTGGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2357
QY 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
DB 2358 CAGGACCGAGGACACATCGACCCCGCTTCGCCAGGGGTGTCTCAAGTGTGACATCTCG 2417
QY 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
DB 2418 GACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2477
QY 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
DB 2478 TATGCCATCAAGACACGCGCGGTGCGCCAGACCTTCAATGAGGCGCAAGCCATTGGCTTC 2537
QY 462 ThrMetTyrThrThrCysIleValTyrPheIleProIlePhePheGlyThrSer 481
DB 2538 ACCATGTACACCACTTGCATCTGTGCTGCGCTTCATCCCATCTCTTTTGGCACCTCG 2597
QY 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
DB 2598 CAGTGGCGCCAGCAAGCTGTATCCAGACGACGCTGACGGTCTCGGTGAGTCTGAGC 2657
QY 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuLeuPheHisPro 521
DB 2658 GCCTCGGTGTCTCTGGGAAATGCTCTACATGCCCAAGTCTACATCATCTCTTCCACCCG 2717
QY 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
DB 2718 GAGCAGAACGTCGCCAAGCGCAAGCGGAGCTCAAGAGCGCTCGTTAGCGCGGCCACCATG 2777
QY 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
DB 2778 TCCAAACAGTTTCAGCAGAAAGGGCACTTCGCGGCCCAACGAGAGAGGCGCAAGTCTGAGCTC 2837
QY 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 581
DB 2838 TGCAGAGAACCTTGNAGGGCCCCCAGCGCTGCGCCACCAACAGACTTACGTTCACCTTACACCAAC 2897
QY 582 HisAlaIle 584
DB 2898 CATGCAATC 2906
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RESULT 9
 PCT-US91-09422-20
 ; Sequence 20, Application PC/TUS9109422
 ; GENERAL INFORMATION:
 ; APPLICANT: Mulvihill, Eileen R.
 ; APPLICANT: Hegen, Frederick S.
 ; APPLICANT: Houamed, Khalid M.
 ; APPLICANT: Almers, Wolfhard
 ; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend
 ; STREET: One Market Plaza, Steuart Street Tower
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105-1492
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/09422
 ; FILING DATE: 19911212
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/672,007
 ; FILING DATE: 18-MAR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/648,481
 ; FILING DATE: 30-JAN-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/626,806
 ; FILING DATE: 12-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 13952-6PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2426 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: SR13
 ; PCT-US91-09422-20

Alignment Scores:

Pred. No.: 4,66e-307 Length: 2426

Score: 2720.50 Matches: 519

Percent Similarity: 90.73% Conservative: 0

Best Local Similarity: 90.73% Mismatches: 1

Query Match: 87.56% Indels: 53

DB: 5 Gaps: 1

US-10-828-332-7 (1-584) x PCT-US91-09422-20 (1-2426)

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QY 14 ----- 14

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QY 14 ----- 14

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QY 14 ----- 14

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QY 14 ----- 14

DB 601 GCTCGCAGGGCCACACAGACCGGCCACCTCTTTTGGATGGGTCTGTATAGCTGGGGCTCC 660

QY 14 ----- 14

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QY 14 ----- 14

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QY 14 ----- 14

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 15 -----GlyPheAspArgTyrPheSerSerArgThrLeuAspAsnAen 28
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 29 ArgArgAsnIleTTPheAlaGluPheTTPGluAspAsnPhHisCysAlaLeuSerArg 48
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 841 CACGCGCTCAAGAGGAGGACCATCAAGAGTGCACCAACCCAGAGGCGCATCGGCGAG 900
 69 AspSerAlaTyrGluGlnGluGlyValGlnPheValIleAspAlaValTyrAlaMet 88
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 109 ArgMetAspProValAspGlyThrGlnLeuLeuLeuTyrIleArgAsnValAsnPheSer 128
 1021 CGCATGGACCCCGTGGATGGGACCCAGCTGCTTAAGTATACATCAGGAACGTCACTCTCA 1080
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 229 CysLeuThrCysProTyrAspMetArgProThrGluAsnArgThrSerCysGlnProIle 248
 1381 TGTAAGACCTGCCCTACGACATGCGGCCACAGAGAACCGCACGAGCTGCCAGGCCATC 1440
 249 ProIleValLeuLeuGluTTPAspSerProTTPAlaValLeuProLeuPheLeuAlaVal 268
 1441 CCCATCGTCAAGTTGGAGTGGAGCTGCGCGTGGCGGCTGTGCTCCCTCTTCTTGGCGGTG 1500
 269 ValGlyIleAlaAlaThrLeuPheValValThrPheValArgTyrAsnAspThrPro 288
 1501 GTGGGATCGCGCGCGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 289 IleValLeuAlaSerGlyArgGluLeuSerTyrValLeuLeuAlaGlyIlePheLeuCys 308
 1561 ATCGTCAAGGCTCGGGCGGAGCTGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 309 TyrAlaThrThrPheLeuMetIleAlaGluProAspLeuGlyThrCysSerLeuArgArg 328
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 329 IlePheLeuGlyLeuGlyMetSerIleTyrAlaAlaLeuLeuThrIleThrAsnArg 348
 1681 ATCTTCTTAGGGCTCGGCATGAGCATGAGTACGCGGCGCTGCTGACCAAGACCAACCGC 1740
 349 IleTyrArgIlePheGluGlnGlyArgSerValSerAlaProArgPheIleSerPro 368

Db 1813 GTGCTGTGTTTGTTCATATTTGGAAATCATCGCCACACCTTTGTGTGTCGTGACCTTT 1872
Qy 282 ValArgTyrAsnAspThrProIleValIleAlaSerGlyArgGluLeuSerTyrValLeu 301
Db 1873 GTCCGCTAATAACACACCTATCGTGAGGCTTCAGGACGCGAACTTAGTTAGCTGCTC 1932
Qy 302 LeuAlaGlyIlePheLeuLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 321
Db 1933 CTACGCGGATTTTCTCTGTTATTCAATCAGCTTTTAAATGATTGCAGCACCATACATA 1992
Qy 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
Db 1993 ATCATATGCTCTTCGACGGGTCTTCAGAGCTTGGATGTGTTTTCAGCTATGAGCC 2052
Qy 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlySerValSer 361
Db 2053 CTTCGTGACCAAAACAAACGTTATCCACCGAATATTGACGAGGGAAGAAATCTGTACA 2112
Qy 362 AlaProArgPheIleSerProIleSerGlnLeuAlaIleThrPheIleLeuLeuSerLeu 381
Db 2113 GCGCCCAAGTTCATTAGTCCAGCATCTCAGCTGGTGATCACCTTCAGCCTCATCTCCGTC 2172
Qy 382 GlnLeuLeuGlyIleCysValThrPheValValAspProSerHisSerValValAspPhe 401
Db 2173 CAGCTCTTGAGGTGTTGTCTGTTGTGTTGTGGATCCGCCCAACATCATCATGACTAT 2232
Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
Db 2233 CGAGACGACGACACTAGATCCAGAGAGCCAGGGAGTCTCAAGTGTGACATTTCT 2292
Qy 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
Db 2293 GATCTCTCACTATTGTTTCACTTGGATACAGTATCTCTTGATGTCTACTTGTACTGTT 2352
Qy 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
Db 2353 TATGCCAATAAACAGAGGTGTCCAGAGCTTTCAATGAAGCCAAACATATGGATT 2412
Qy 462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 481
Db 2413 ACCATGTATACCATCGCATCATTTGGTTAGCTTTTCATCCCATCTTTTGTGTACAGCC 2472
Qy 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
Db 2473 CAGTCAGCAGAAAGATGTACATCCAGACACAACTTACTGTCTCTCCATGAGTTAAGT 2532
Qy 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuLeuPheHisPro 521
Db 2533 GCTTCAGTATCTCTGGCATGCTCTATATGCCCAAGGTTTATATATATTTTTCATCCA 2592
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
Db 2593 GAACAGATGTTCAAAAGCAGAGGAGCTTCAAGGCTGTGTGTGACAGCTGCCACCATG 2652
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 2653 CAAGCAAACTGATCCAAAGAGAAATGACAGACCAATATGGCGAGTGAAGAGTGAATC 2712
Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 581
Db 2713 TGTGAGGCTTTGAACCAACCACTCTCTTACCAAGACACATATATATGTTTACAGCAAT 2772
Qy 582 HisAlaIle 584
Db 2773 CATTCATC 2781

RESULT 11

US-08-855-146-3

; Sequence 3, Application US/08855146

; Patent No. 6221609

; GENERAL INFORMATION:

; APPLICANT: Belagaje, Rama M.

; APPLICANT: Wu, Su

; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Department
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,146
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,243
; FILING DATE: 07-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10836
; TELEPHONE: (317) 276-6334
; TELEFAX: (317) 276-2764
; INFORMATION FOR SEQ ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; US-08-855-146-3

Alignment Scores:
Pred. No.: 7,778-266 Length: 3321
Score: 2370.00 Matches: 437
Percent Similarity: 84.91% Conservative: 58
Best Local Similarity: 74.96% Mismatches: 86
Query Match: 76.28% Indels: 2
DB: 3 Gaps: 2

US-10-828-332-7 (1-584) x US-08-855-146-3 (1-3321)

Qy 3 GlyValSerSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 1036 GGGGCGUGACAAUUUUGCCCAACGACCAUUGAUGAUCUUGAUCUUGAUCUUGA 1095
Qy 22 SerArgThrLeuAspAsnArgArgAsnIleTTPheAlaGluPheTTPGluAspAsn 41
Db 1096 AGCCGAAACUUGCCCAUUAUCGAAAGAAUUGUGUGUUUGAGAAUUCUGGGAGGAU 1155
Qy 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
Db 1156 UUGGCGUCAGUAGGACUACUAGG---AAAGACACAGUACAUAAAGAAUAGCACA 1212
Qy 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGlnGlyLysValGlnPheVal 81
Db 1213 GGGCUGGAGCGAAUUGCUGCGGAUUCUUAUGAACAGGAGGAAAGGCUCAUUGUA 1272
Qy 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
Db 1273 AUUGAUGCUGUAUUAUCCCAUGGCUUACGCCUUGCAUUAUGCAAAAGAUUCUGCCCU 1332
Qy 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysTyr 121
Db 1333 GGAUACAUGGCUUUGUCCAGGAUGAGUACCAUUGAUGGAGGAAAGACUACUUGUUAU 1392
Qy 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141

1393 AUUCGGGCUUAUUUAUAGGCGAGUCGCGCACUCCUGUCACUUUUUAUUGAAAAACGGA 1452
142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
1453 GAUGCUCUGGACGUAUGAUUAUCUCCAGUAUCAAUAACCAAAAGACACAGAGUAC 1512
162 LysValIleGlySerThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 181
1513 AAAGUCAUGCGCCACUGACCAUUCAGCUUUAUUAAGGUGGAAGACAUAGCAGUGGCU 1572
182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
1573 CAUAGAGAACAUAUCUACCCGCGGUCUGUCGAGCCGUGUAAGCCAGGCGAGAGG 1632
202 LysIleThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 221
1633 AAGAAACCGUGAAGGGGUCUUGCUGGCGACUUGGAACGUGGAAGGUAAGGUUACAAC 1692
222 TyrGlnValAspArgTyrThrCysIleThrCysProTyrAspMetArgProThrGluAsn 241
1693 UACGAGGUGGAGAGCUGUCUGGUAACUUGGCCUUGGAGUCAGACCAACCAUAGAAC 1752
242 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 261
1753 CGCAGCGCGCCAGCUUAUCCCAUACAUAUUGAGUGGCAUUCUCCUGGCGUG 1812
262 LeuProLeuPheLeuAlaValValGlyIleAlaIleAlaThrLeuPheValValThrPhe 281
1813 GUGCUGUGUUGUUGCAUAUUGGAAUAUCGACCAUCCUUGUGAUGUGGACCCUUU 1872
282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
1873 GUCCGCUAUAUGACACACCUUAGGUGGCGUCCAGGACCGAUCUUGUUAUGUGUC 1932
302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
1933 CUACGGGGAUUUUUCUUGUAUUAUCAUCAGUUUUUAUUGAGCAGCAGACCAUAUA 1992
322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
1993 AUCAUAUGCUCUUCGCGGCGUCCUCCAGGACUUGGCAUGUGUUAUUGCAGCAGCC 2052
342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLeuArgSerValSer 361
2053 CUUCUGACCAAAACAAACCGUAUCCAGCAUAUUGAGCAGGGAAGAAUUCUGUCACA 2112
362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
2113 GCGCCCAAGUAUUAUUGCAGCAUCUCCAGGUGGUAUCCUCCAGCUCUCCGUC 2172
382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401
2173 CAGCUCUUGGAGUGUUGUCUGUUGUUGGUAUCCCGCCCAUACAUAUUGACUUAU 2232
402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
2233 GGAGAGCAGCGGACACUAGUCCAGAGAAAGCGCAGGAGGUGUCUUAAGUGGACAUUU 2292
422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
2293 GAUCUCUACAUAUUUGUUAUUGGUAUAGUAUCCUUGAUGGUGGACUUGUUAUUG 2352
442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
2353 UAUGCCAAUAAAACGAGAGGUGUCCAGAGCUUUAUUGAAGGCAACCAUUAUUGGAUU 2412
462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 481
2413 ACCAUGUAUACCCUCCGUAUUAUUGGUAUUGGUAUCCCAUCCUUAUUGGUAUAGCC 2472
482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501

2473 CAGUCAGCAGAAAAAGUAUGUAUCCAGACAACACUAUCUGUCUCCAGAGUUUAAGU 2532
502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521
2533 GCUUCAGUAUCUCUGGCGAUGUCUAUAGCCCAAGGUUUUAUUAUUAUUUUUAUCCA 2592
522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
2593 GAACAGAAUGUCAAACAAACGCAAGAGGAGGCUCAAGGCGUGGUGGACAGCUGCCACCAUG 2652
542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
2653 CAAGCAAAACUGAUCCAAAGGAAAUAGACAGACCAAAUUGCGAGGUAAGUAGAACUC 2712
562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 581
2713 UGUGAGAGUCUUGAAACCAACACUUCUCCUCCAGCAACAUAUAUACAGUUACAGCAAU 2772
582 HisAlaIle 584
2773 CAUCAAUC 2781

RESULT 12
US-08-823-110-2
; Sequence 2, Application US/08823110
; Patent No. 6077675
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,110
; FILING DATE: March 24, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,298
; FILING DATE: February 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-823-110-2

Alignment Scores: 3.74e-263 Length: 3833
Pred. No.:

Score: 2348.00 Matches: 438
Percent Similarity: 82.56% Conservatives: 59
Best Local Similarity: 72.76% Mismatches: 84
Query Match: 75.57% Indels: 21
DB: 3 Gaps: 3

US-10-828-332-7 (1-584) x US-08-823-110-2 (1-3833)

QY 3 GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 1494 GGGGGTGTGACAAATTTGGCCAAACGAGCATCAATATGATGGATTTGATCGATCTTTAGA 1553
QY 22 SerArgThrLeuAspAsnAsnArgAsnIleTTPheAlaGluPheTTPGluAspAsn 41
Db 1554 AGCCGAACCTCTGGCCAAATATCGAAGAAATGTGTGTTTGCAGAAATCTCTGGGAGAGAAAT 1613
QY 42 PheHisCysLeuSerArgHisAlaLeuLeuLysGlySerHisIleLysLysCysThr 61
Db 1614 TTTGGCTGCAGTTAGGATCATATGGG---AAAGGAACAGTCATATAAAGAAATGCACA 1670
QY 62 AsnArgGluArgIleGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 81
Db 1671 GGGCTGGAGCGAATTCCTCGGATTCATCTTATGAACAGGAAGGAAGGTCCAAATTTGTA 1730
QY 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
Db 1731 ATTGATGCTGTATATTCACATGGCTTACGCCCTGCACAAATATGCACAAAGATCTCTGCCCT 1790
QY 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
Db 1791 GGATACATTTGGCTTTTCCAGATAGTACATTTGATGGGAAGAGAGCTACTTGGTTAT 1850
QY 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
Db 1851 ATTGGGCTGTAAATTTTAAATGGCAGTGTGGCCTCTCTGTCATCTTTTAAATGAACCGA 1910
QY 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
Db 1911 GATGCTCTGGACGTTATGATATCTCCAGTATCAATTAACCAACCAAAAGACAGAGTAC 1970
QY 162 LysValIleGlySerTyrThrAspHisLeuHisLeuArgIleGluArgMetGlnTyrPro 181
Db 1971 AANGTCATCGGCACCTGGACCAATCAGCTTTCATTAAGTGTGAAGACATGACGTGGCT 2030
QY 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
Db 2031 CATAGAACATACCTCACCGCGCTGTCTCGACGCTGCCGTGTGAAGCCAGGGAGG 2090
QY 202 LysLysThrValLysGlyMetAlaCysCysTTPHisCysGluProCysThrGlyTyrGln 221
Db 2091 AAGAAAAACGGTGAAGGGTCCCTTGTCTGCTGGCACCTGTGAACGCTGTGAAGCTTACAAC 2150
QY 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
Db 2151 TACCAGGTGGATGAGCTGCTGTGAACCTTTGCCCTCTGGATCAGAGACCCCAACATGAAC 2210
QY 242 ArgThrSerCysGlnProIleProIleValLysLeuGluTyrAspSerProTyrAlaVal 261
Db 2211 CGCACAGGCTGCAGCTTATCCCATCATCAATTTGGAGTGGCATTTCTCCCTGGGCTGTG 2270
QY 262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 281
Db 2271 GTGCCCTGTGTTTGTGCAATATTTGGAAATCATCGCCACCCACCTTTGTGATCGTGACCTT 2330
QY 282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
Db 2331 GTCCCTGTATTAATGACACCTATCTGAGGGCTTACAGGACCGCACTTAGTTACGTGCTC 2390
QY 302 LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 321
Db 2391 CTAAACGGGATTTTCTCTGTTATTCATCAGCTTTTATGATTTGCACCAAGATACA 2450
QY 322 GlyThrCysSerLeuArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341

Db 2451 ATCATATGCTCTCTCCGACGGGTCTTCTTAGAAGCTTGGCATTTGTTTCAAGCTATGACGCC 2510
QY 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
Db 2511 CTTCTGACCAAAACAAACCGTATCCACGATATTTGAGCAGGGGAAGAAATCTGTCA 2570
QY 362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
Db 2571 GCGCCCAAGTTTCAATAGTCCAGCATCTCAGCTGGTGATCACCTTCAGCCCTCATCTCCGTC 2630
QY 382 GlnLeuLeuGlyIleCysValTyrPheValValAspProSerHisSerValValAspPhe 401
Db 2631 CAGCTCTTGGAGTGTGTCTGGTTTGTGTGGATCCCCCAATCATCATCATGACTAT 2690
QY 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
Db 2691 GGAGAGCAGCGGACACTAGATCCAGAGAAGCCAGGGAGTCTCAAGTGTGCACATTTCT 2750
QY 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
Db 2751 GATCTCTCACTCAATTTGTTCACTTGGATACAGTATCTCTTGTGATGGTCACTTGTACTGT 2810
QY 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
Db 2811 TATGCCATTAACGAGAGGTGTCCAGAGACTTTTCAATGAAGCCAAACCTTATTGGATT 2870
QY 462 ThrMetTyrThrThrCysIleValTyrLeuAlaPheIleProIlePhePheGlyThrSer 481
Db 2871 ACCATGATATACCATCTGTCATCATTTGGTTAGCTTTTCCATCCCATCTTTTGTGACAGCC 2930
QY 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 501
Db 2931 CAGTCAGCAAAAAGATGTACATCCAGACAACACACTTACTGTCTCCATGATGTTAAGT 2990
QY 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521
Db 2991 GCTTCAGTATCTCTGGGATGCTCTATATGCCAAGGTTTATATATATATTTTTCATCCA 3050
QY 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
Db 3051 GAACAGATGTTCAAAAACGCAAGAGAGCTTCAAGGCTGTGTGACAGCTGCCACCATG 3110
QY 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 3111 CAAGCAAACTGATCCAAAAAGGAAATGACAGACCAATGGCAGGTGAAAAAGTGAATC 3170
QY 562 CysGluAsnLeuGluThrProAla----- 569
Db 3171 TGTGAGAGTCTTGAACCAACCAAGTAAAGTCATCTGTAGAGTTTCCGATGGTCAAGACGGG 3230
QY 570 -----Leu-AlaThrLysGlnThrTyrValThrTyrThrAsnHisAl 583
Db 3231 AGCACTTCTAATAGATCTTCTCTACCAAGACACATATATCATGTTACAGCAATCATTC 3290
QY 583 aile 584
Db 3291 AATC 3294

RESULT 13
US-08-604-298-2
; Sequence 2, Application US/08604298
; Patent No. 6084084
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,298
FILING DATE: February 21, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-604-298-2

Alignment Scores:

Pred. No.:	3,746-263	Length:	3833
Score:	2348.00	Matches:	438
Percent Similarity:	82.56%	Conservative:	59
Best Local Similarity:	72.76%	Mismatches:	84
Query Match:	75.57%	Indels:	21
DB:	3	Gaps:	3

US-10-828-332-7 (1-584) x US-08-604-298-2 (1-3833)

Qy	3	GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer	21
Db	1494	GGGGCTGTGACAAATTTTGGCCAAACGACGATCAATTTGATGGATTTGATCGATACTTTTGA	1553
Qy	22	SerArgThrLeuAspAsnArgArgAsnIletrPheAlaGluPheTrpGluAspAsn	41
Db	1554	AGCCGAACTCTTCCCAATTAATCGAAGAATGTGTGTTTGCAGAAATCTCGGAGAGGAT	1613
Qy	42	PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysCysThr	61
Db	1614	TTTGCTGCAAGTTAGGATTCATCGGG---AAAGGAACAGTCATATAAGAAATGCACA	1670
Qy	62	AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal	81
Db	1671	GGGCTGGAGCGCAATTTGCTCGGGATTCATCTTATGAACAGGAAGGAAAGGTCCTCAATTTGTA	1730
Qy	82	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	101
Db	1731	ATTGATGCTGATATTTCCATGGCTTACCGCCCTGCACAAATATGCACAAAGATCTCTGCCCT	1790
Qy	102	GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysTyr	121
Db	1791	GGATACATTGGCTTTGTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT	1850
Qy	122	IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly	141
Db	1851	ATTCGGGCTGTAAATTTTAAATGGCAGTCTGGCAGTCTGGCAGTCTGGCAGTCTGGCAG	1910

Qy	142	AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr	161
Db	1911	GATGCTCTCGACGTTATGATATCTTCAGTATCAAAATACCAACAAAGACACAGATAC	1970
Qy	162	LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro	181
Db	1971	AAAGTCATCGGCCACTCGACCAATCAGCTTCATCTAAAGTGGAGACATCGATGGGCT	2030
Qy	182	GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg	201
Db	2031	CATAGAGAACATCTACCCGGGCTCTGTCTGACGCTCGGTGTAGACCCAGGAGAGG	2090
Qy	202	LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln	221
Db	2091	AAGAAAAGGTTGAAAGGGGCTCTGCTGGCAGTGTGAACGCTGTGAAGGTTACAAC	2150
Qy	222	TyrGlnValAspArgTyrThrCysLysThrCysProTrpAspMetArgProThrGluAsn	241
Db	2151	TACCAGGTGGATGAGCTGTCTGTGAACCTTTGGCCCTCTGGATCAGAGACCCAAACATGAAC	2210
Qy	242	ArgThrSerCysGlnProIleValLysLeuGluTrpAspSerProTrpAlaVal	261
Db	2211	CGACAGGCTGCCAGCTTATCCCATCATCAATTTGAGTGGCATTTCTCCCTGGGCTGTG	2270
Qy	262	LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe	281
Db	2271	GTGCTGTGTTTGTTCATATTGGGAATCATGCCACACACCTTTGTGTGCTGACCTTT	2330
Qy	282	ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu	301
Db	2331	GTCCGCTATAATGACACACCTATCGTGGGGCTTTCAGGACGCGAATTTAGTTAGTGTCTC	2390
Qy	302	LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu	321
Db	2391	CTAACGGGGATTTTCTCTGTTATTCATCAGCTTTTATGATGACGACACAGATACA	2450
Qy	322	GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla	341
Db	2451	ATCATATGCTCTTCCGACGGCTCTCTAGGACTTGGCATGTGTTTCAGCTATGACGCC	2510
Qy	342	LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer	361
Db	2511	CTTCTGACCAAAACCAACCGTATCCACGAAATTTTCAGGACGAGGGAAGAATCTGTGCTC	2570
Qy	362	AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu	381
Db	2571	GGCCCCAAGTTTCATAGTCCAGCATCTCAGCTGGTGATCACCTTCAGCCTCATCTCCGTC	2630
Qy	382	GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe	401
Db	2631	CAGCTCTTGGAGTGTGTGTCTGGTTTGTGGATCCCCCACCACATCATCATTTGACTAT	2690
Qy	402	GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer	421
Db	2691	GGAGAGCAGCGGACACTAGATCCAGAGAGCCAGGCGGAGTGTCTCAAGTGTGACATTTCT	2750
Qy	422	AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal	441
Db	2751	GATCTCTCATCTTTGTTTCTGTTGATACAGTATCTCTTGTATGGTTCATCTTGTACTGTT	2810
Qy	442	TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe	461
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[illegible]

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RESULT 14
US-08-823-110-5
; Sequence 5, Application US/08823110
; Patent No. 6077675
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
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,  
CURRENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
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/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
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/ MEDIUM TYPE: storage
/
/ COMPUTER: IBM Compatible
/
/ OPERATING SYSTEM: IBM P.C. DOS 5.0.0
/
/ SOFTWARE: PatSeq for Windows 2.0
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/823,110
/
/ FILING DATE: March 24, 1997
/

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/604,298
FILING DATE: February 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/259
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

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; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-823-110-5

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US-08-823-110-5

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Best Local Similarity:	75.97%	Mismatches:	81
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DB:	3	Gaps:	2

US-10-828-332-7 (1-584) x US-08-823-110-5 (1-2724)			
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Qy	22	SerArgThrLeuAspAsnAsnArgArgAsnIleTrpPheIaGluPheTrpGluAspAsn	41
Db	1039	AGCCGAACCTCTGCCAATAATCGAAGAAATGTGTGGTTTCAGAAATTTCTCGGAGGAGAAT	1098
Qy	42	PheHisCysValysLeuSerArgHisAlaLeuLeuLysGlySerHisIleLysLysCysThr	61
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Qy	62	AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal	81
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Qy	82	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	101
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Qy 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
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Qy 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
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Qy 382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401
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Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
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Job time : 333 secs

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2005, 08:56:12 ; Search time 7314 Seconds
(without alignments)
3868.997 Million cell updates/sec

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Perfect score: 3107
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3050.5	98.2	3704	10	RATMGLURD
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4	3023.5	97.3	4425	10	BC072635

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25	2547.5	82.0	3002	10	BC080284
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ACCESSION	AR381454	AR381454	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
VERSION	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
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SOURCE	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
ORGANISM	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
REFERENCE	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
AUTHORS	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
TITLE	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
JOURNAL	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
FEATURES	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
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Alignment Scores:	3.16e-246	Length:	2838
Pred. No.:	3050.50	Matches:	575
Score:	98.97%	Conservative:	2
Percent Similarity:	98.63%	Mismatches:	5
Best Local Similarity:	98.18%	Indels:	1
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US-10-828-332-7 (1-584) x AR381454 (1-2838)

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Db 1452 GACTGTCTCTCATCTGCCCTGCTGGGTACAGCATGTCTGATGGTCAAGTGGTACTGTG 1511
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Db 1572 ACCATGTACACCACTGCTGCTGGCTGGCTTCAATCCCATCTTTTGGCACCTCA 1631
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Qy 502 AlaserValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro 521
Db 1692 GCTTCAGTGTCCCTGGGGATGCTCTACATGCCAAAGTCTACATCATCTCTCCACCG 1751
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
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Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrAsn 581
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RESULT 2
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LOCUS Rat metabotropic glutamate receptor 4 mRNA, primary transcript.
DEFINITION M92077
ACCESSION M92077
VERSION M92077.1 GI:205403
KEYWORDS glutamate receptor; metabotropic glutamate receptor.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 3704)
AUTHORS Tanabe,Y., Masu,M., Ishii,T., Shigemoto,R. and Nakanishi,S.
TITLE A family of metabotropic glutamate receptors
JOURNAL Neuron 8 (1), 169-179 (1992)
MEDLINE 92110002
PUBMED 1309649
COMMENT Original source text: Rattus norvegicus (strain Sprague-Dawley)
adult cDNA to mRNA.
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US-10-828-332-7 (1-584) x RATMGLURBD (1-3704)

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QY 14 ----- 14
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QY 15 -----GlyPheAspArgTyrPheSerSerArgThrLeuAspAsnAan 28
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QY 109 ArgMetAspProValAspGlyThrGlnLeuLysTyrIleArgAsnValAsnPheSer 128
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RESULT 3

RATMGLUR4A

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QY 289 IleValLysAlaSerGlyArgGluLeuSerTyrValLeuLeuAlaGlyLysPheLeuCys 308
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QY 309 TyrAlaThrThrPheLeuMetIleAlaGluProAspLeuGlyThrCysSerLeuArgArg 328
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QY 369 AlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeuGlnLeuLeuGlyIleCysVal 388
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LOCUS	RATMGLUR4A	4488 bp	mRNA	linear	ROD 01-APR-1996
DEFINITION	Rat metabotropic glutamate receptor (GLUR4) mRNA, complete cds.				
ACCESSION	M90518				
VERSION	M90518.1	GI:205400			
KEYWORDS	metabotropic glutamate receptor.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
REFERENCE	1 (bases 1 to 4488)				
AUTHORS	O'Hara, P.J., Sheppard, P.O., Thøgersen, H., Venezia, D., Haldeman, B.A., McGrane, V., Houamed, K.M., Thomsen, C., Gilbert, T.L. and Mulvihill, E.R.				
TITLE	The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins				
JOURNAL	Neuron 11 (1), 41-52 (1993)				
MEDLINE	93332699				
PUBMED	8338667				
REFERENCE	2 (bases 1 to 4488)				
AUTHORS	O'Hara, P.J.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-APR-1992) Patrick J. O'Hara, ZymoGenetics, Inc., Seattle, WA 98105, USA				
COMMENT	Original source text: Rattus norvegicus cDNA to mRNA.				
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ORIGIN					
Alignment Scores:					
Pred. No.:	5.85e-246	Length:	4488		
Score:	3050.50	Matches:	583		
Percent Similarity:	91.67%	Conservative:	0		
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 DEFINITION Mus musculus cDNA clone IMAGE:6850174, partial cds.
 ACCESSION BC072635
 VERSION BC072635.1 GI:49257159
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 4425)
 REFERENCE Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,
 Schnercher, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 2 (bases 1 to 4425)
 REFERENCE Strausberg, R.
 DIRECT SUBMISSION
 TITLE
 JOURNAL
 JOURNAL
 REMARK
 COMMENT
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
 Thomas L. Casavant.
 Web site: <http://genome.uiowa.edu>
 Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
 Ronaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
 Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
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 Clone distribution: MGC clone distribution information can be found
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Db 3053 TATGCCATCAAGACTCGAGGGCTGCGCTGAGACCTTCAATGAGGCAAGCCCATCGGCTTC 3112
Qy 462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 481
Db 3113 ACCATGTACACCCTGCATGCTGCTGGCTTTCATCCCATCTTTTGGCACCTCG 3172
Qy 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
Db 3173 CAGTGGGCTGACAAGCTGTATCATCCAGAACACACTGACGGTCTCTGTGAGTCTGAGC 3232
Qy 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521
Db 3233 GCTTCAGTGTCCCTGGGGATGCTCTACATGCCAAAGCTACATCATCTCTTCCACCCG 3292
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
Db 3293 GAGCAGAACGTGCCAAGCGCAGCGAGCGCTCAAGCCGTTGTACCGCGCCACCATG 3352
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 3353 TCCAACAAGTTCAACAGAAAGGGCACTTCAGGCTTAATGGGGAAGCCAAAGTCAGAGCTG 3412
Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 581
Db 3413 TGTGAGAACCTGGAGGCGCCCGACGACCTGCCCAACAGACCTACGTCACCTTACCCAAC 3472
Qy 582 HisAlaIle 584
Db 3473 CATGCAATC 3481

RESULT 5
LOCUS AR149574 2736 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6228610.
ACCESSION AR149574
VERSION AR149574.1 GI:15114165
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2736)
AUTHORS Flor,P.Josef., Kuhn,R., Lindauer,K., Puttner,I. and Knopfel,T.
TITLE Human metabotropic glutamate receptor subtypes (hmr4, hmr6, hmr7)
and related DNA compounds
JOURNAL Patent: US 6228610-A 1 08-MAY-2001;
FEATURES
source Location/Qualifiers
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ORIGIN

Alignment Scores: 2.21e-242 Length: 2736
Pred. No.: 3004.50 Matches: 564
Score: 3004.50 Conservative: 6
Percent Similarity: 97.77% Mismatches: 12
Best Local Similarity: 96.74% Indels: 1
Query Match: 96.70% Gaps: 1
DB: 6

US-10-828-332-7 (1-584) x AR149574 (1-2736)
Qy 3 GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
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Qy 22 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 41
Db 1048 AGCCGCAAGCTGGGCAACACCGCGCAACATCTGGTTTGGCCGAGTTCCTGGGAGGACAAC 1107
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DB 1108 TTCCATGCAAGCTGAGCGCCACCGCCTCAAGAAGGCGAGCCACGCTCAAGAAGTGACCC 1167

QY 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyValGlnPheVal 81
DB 1168 AACCGTGACGAATTTGGGCGAGATTGAGCTTATGAGCAGAGGAGGAGGTGAGTTTGG 1227

QY 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
DB 1228 ATCGATGCCGTGTAGCCATGGCCATGGCCAGCGCTGCAGCCCATGCACCGTACCTGTGCCC 1287

QY 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
DB 1288 GGCCCGGTGGGGCTCTGCGCCGCGCATGGACCTGTAGATGGCACCAGCTGTCTAAGTAC 1347

QY 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
DB 1348 ATCCGAACGTCACCTTCTCAGCATGCGGAGGAACTCTGTGACCTTCAATGAGATGGA 1407

QY 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
DB 1408 GATGCGCTGGGGCTATGACATCTACCAATACCGAGCTGCGCAAGATTCTGCCGAGTAC 1467

QY 162 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 181
DB 1468 AAGGTCAATGGCTCTCTGGACTGACCACCTGCACCTTAGAATAGCGGATGCACTGGCGG 1527

QY 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
DB 1528 GGGAGCGGGCAGCAGCTGCGCCCGCTCCATCTCAGCGCTGCCCTGCCAACCGGGTGAGCGG 1587

QY 202 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 221
DB 1588 AAGAAGACAGTGAAGGGCATGCTTGTCTGGCATCTGCGAGCCTTGCAAGGGTACCAG 1647

QY 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
DB 1648 TACCAGGTGGACCGGTACACCTGTGAAGAGCTGTCTCTATGATCATCGCGCCACAGAGA 1707

QY 242 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 261
DB 1708 CGCAGCGGCTGCGCGCCCATCCCATCATCAAGCTTGAAGTGGGGCTGCGCCCTGGGCGGTG 1767

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DB 1768 CTGCCCCCTTCTCTGGCGGTGGTGGCATCGCTGCACGTTGTTCTGGTGATCACCTTT 1827

QY 282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
DB 1828 GTGCGCTACAAACGACACGCGCCATCGTCAAGGCTCGGCGGTGAACCTGAGCTACGTCGTG 1887

QY 302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
DB 1888 CTGGCAGGATCTCTCTGTGCTATGCCACCATCTTCTCATGATCGCTGAGCGCGACCTT 1947

QY 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
DB 1948 GGCACCTGCTGCTGCGCGGAATCTTCTGGAGCTAGGGATGAGCATCAGCTATGCAGCC 2007

QY 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
DB 2008 CTGCTCACCAAGACCAACCGCATCTACCGCATCTTCGAGCAGGCGCAAGGCTCGGTCACT 2067

QY 362 AlaProArgPheIleSerProIleSerGlnLeuAlaIleThrPheIleLeuLeuSerLeu 381
DB 2068 GCGCCACGCTTCATCAGCGCGCCCTCACAGCTGGCCATCACCTTCAGCTCATCTCGCTG 2127

QY 382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401
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QY 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
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QY 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
DB 2248 GACCTGTGCTCATCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2307

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QY 462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 481
DB 2368 ACCATGTACACCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2427

QY 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
DB 2428 CAGTGGCGGACCAAGCTGTATCATCAGACGACGACGCTGTGCTGTGCTGTGCTGTGCTGTG 2487

QY 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521
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QY 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
DB 2548 GAGCAGAACGTCGCCCAAGCGCAAGCGCAGCTCAAAGCGCTGCTTACGCGCGCCACCATG 2607

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QY 582 HisAlaIle 584
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RESULT 6
A43637
LOCUS A43637 2738 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 1 from Patent WO9508627.
ACCESSION A43637
VERSION A43637.1 GI:2298839
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2738)
AUTHORS Flor, P. J., Kuhn, R., Lindauer, K., Puettner, I., and Knoepfel, T.
TITLE HUMAN METABOTROPIC GLUTAMATE RECEPTOR SUBTYPES (HMR4, HMR6, HMR7)
AND RELATED DNA COMPOUNDS
JOURNAL Patent: WO 9508627-A 1 30-MAR-1995;
COMMENT CIBA GEIGY AG (CH)
Other publication CA 2171206 950330
Other publication NO 961115 960319
Other publication FI 961251 960318
Other publication AU 7615994 950410.
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ORIGIN

Alignment Scores:
Pred. No.: 2,21e-242 Length: 2738
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 6 Gaps: 1

US-10-828-332-7 (1-584) x A43637 (1-2738)

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Db	1048	AGCCGACGCTGGACAAACAACCGCGCAACATCTGGTTTCCGAGTCTCGGAGGACAAC	1107
Qy	42	PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr	61
Db	1108	TTCCACTGCAAGCTGAGCGCGCACGCCCTCAAGAAGGGCAGCCACGTCAGAGTGCACC	1167
Qy	62	AsnArgGluArgIleGlyClnAspSerAlaTrpGluGlnGluGlyValGlnPheVal	81
Db	1168	AACCGTAGCGAAATTTGGCAGGATTCACGCTATTAGCAGGAGGGAGGTCAGTTTGTG	1227
Qy	82	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	101
Db	1228	ATCGATGCGGTGTAGCCCATGGCCACGCGCTGCACGCCATGCACCGTGACTGTGTCCC	1287
Qy	102	GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr	121
Db	1288	GGCCGCGTGGGCGCTCTGCCCGCATGACCCCTGTAGATGGCACCCACGCTGTTAAGTAC	1347
Qy	122	IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly	141
Db	1348	ATCCGAAACGTCACCTCTCAGGCATCCGAGGGAACCTGTGACCTTCATAGAGATGGA	1407
Qy	142	AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr	161
Db	1408	GATGCGCTGGCGGTATGACATCTACCAATACGAGCTGGCAACGATTCCTGCCGAGTAC	1467
Qy	162	LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro	181
Db	1468	AAGGTCATTGGCTCTCGGACTGACCACTGACCTTAGAATAGCGCGATGCACCTGGCGG	1527
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Db	1528	GGGAGCGGGCAGCAGCTCCCGCGCTCCATCTGCGAGCCTGCCCCGTCGCAACCGGGTGAGCGG	1587
Qy	202	LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln	221
Db	1588	AGAAGAAGAGTGAAGGGCATGCCTTGCTGCTGGCACTCGGAGCCTTGACAGGGGTACCAG	1647
Qy	222	TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn	241
Db	1648	TACCAGTGGGACCGCTACACCTGTAAAGACGTGTCCCTATGACATGCGGCCACACAGAAC	1707

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Qy	242	ArgThrSerCysGlnProIlePheValLysLeuGluTrpAspSerProTrpAlaVal	261
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Qy	262	LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValValThrPhe	281
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Qy	282	ValArgTyrAsnAspThrProIleValLysAlaSerGlyValArgGluLeuSerTyrValLeu	301
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Qy	302	LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu	321
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Qy	322	GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla	341
Db	1948	GGCACCTGCTCGCTGCGCGCAATCTTCTGGGATAGGATAGGCATCAGCTATGCAGCC	2007
Qy	342	LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer	361
Db	2008	CTGCTCAACCAAGCAACACCGCATCTACCGCATCTTCGAGCAGGCAAGCGCTCGGTGAGT	2067
Qy	362	AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu	381
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Qy	382	GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe	401
Db	2128	CAGCTGCTGGGCATCTGT	2187
Qy	402	GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer	421
Db	2188	CAGACCGAGGACACTCGACCCCCGCTTCGCCAGGGGTGTGCTCAAGTGTGACATCTCG	2247
Qy	422	AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal	441
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Qy	442	TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe	461
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Qy	462	ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer	481
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Qy	482	GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer	501
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Qy	522	GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet	541
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Qy	542	SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu	561
Db	2608	TCCAACAGTTTACGACAGAGGGCACTTCCGGCCCCAACCGAGAGGCCAAGTCTGAGCTC	2667
Qy	562	CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn	581
Db	2668	TGCAGAACCTTGAGGCCCCAGCGCTGCCCAACACAGACTTACGTCACTTACACCAAC	2727
Qy	582	HisAlaIle	584
Db	2728	CATGCAATC	2736

AX427263
LOCUS AX427263 2738 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent EP1199359.
ACCESSION AX427263
VERSION AX427263.1 GI:21530616
SOURCE unidentified
ORGANISM unidentified
unclassified.
1
REFERENCE
AUTHORS Flor,P.J., Kuhn,R., Lindauer,K., Puettner,I. and Knoepfel,T.
TITLE Human metabotropic glutamate receptor subtypes (hmr4, hmr5, hmr7)
and related dna compounds
JOURNAL Patent: EP 1199359-A 1 24-APR-2002;
Novartis AG (CH)
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ORIGIN

Alignment Scores:
Pred. No.: 2,216-242 Length: 2738
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 6 Gaps: 1

US-10-828-332-7 (1-584) x AX427263 (1-2738)

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Db 1048 AGCCCAAGCTGGACCAACACCGCGCAACATCTGCTTTGCCAGTTCCTGGAGGACAAC 1107
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Db 1108 TTCCATGCAAGCTGAGCGCCACCGCTCAAGAGAGGCGAGCCAGTCAAGAGGTGAC 1167
Qy 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 81
Db 1168 AACCGTGAGCGAATTTGGGCGAGATTTCAGCTTATGACGAGGAGGAGGAGTTCGTTGTG 1227
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Db 1228 ATCGATCGCGTGTACGCCATGCGCCACCGCTGCGACCGCATGACCGGTGTCCTCC 1287

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ACCESSION AKI22982
VERSION AKI22982.1 GI:34528429
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Sekine, M., Oabayashi, M., Nishi, T., Shibahara, T., Tanaka, H.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Negahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuna, M.,
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Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
TITLE
JOURNAL
PUBMED

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2 Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hiraoka, M.,
Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K.,
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Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
Unpublished
NEDO human cDNA sequencing project
3 (bases 1 to 3176)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(8-mail:genomes@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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ACCESSION AR208972
VERSION AR208972.1 GI:21510266
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 3431)
AUTHORS Belagaje,R.M. and Wu,S.
TITLE Metabotropic glutamate receptor 4 nucleic acid
JOURNAL Patent: US 6384205-A 1 07-MAY-2002;
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Location/Qualifiers
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DEFINITION Sequence 3 from patent US 6384205.
ACCESSION AR208973
VERSION AR208973.1 GI:21510267
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3431)
AUTHORS Belagaje,R.M. and Wu,S.
TITLE Metabotropic glutamate receptor 4 nucleic acid
JOURNAL Patent: US 6384205-A 3 07-MAY-2002;
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LOCUS Human metabotropic glutamate receptor 4 mRNA, complete cds.
DEFINITION U92457
ACCESSION U92457
VERSION U92457.1 GI:1935038
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3431)
AUTHORS Wu, S., Wright, R. A., Rockey, P. K., Burgett, S. G., Arnold, J. S.,
Rostek, P. R., Jr., Johnson, B. G., Schoepf, D. D. and Belagaje, R. M.
TITLE Group III human metabotropic glutamate receptors 4, 7 and 8:
molecular cloning, functional expression, and comparison of
pharmacological properties in RGT cells
JOURNAL Brain Res. Mol. Brain Res. 53 (1-2), 88-97 (1998)
MEDLINE 98141892
PUBMED 9473604
REFERENCE 2 (bases 1 to 3431)
AUTHORS Wu, S. and Belagaje, R. M.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-1997) mc625, Eli Lilly and Company, Lilly
Corporate Center, Indianapolis, IN 46285, USA
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ORIGIN

Alignment Scores:

Pred. No.: 2,996-242 Length: 3431
 Score: 3004.50 Matches: 564
 Percent Similarity: 97.77% Conservative: 6
 Best Local Similarity: 96.74% Mismatches: 12
 Query Match: 96.70% Indels: 1
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US-10-828-332-7 (1-584) x HSU92457 (1-3431)

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Qy	42	PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysCysThr	61		
Db	1133	TTCCACTGCAAGCTGAGCGCGCACCCCTCAAGAAAGGCGACCGCTCAAGAAAGTGCAAC	1192		
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RESULT 12

AK122836

LOCUS

DEFINITION

to Metabotropic glutamate receptor 4 precursor.

ACCESSION

3850 bp mRNA linear PRI 30-JAN-2004
 Homo sapiens cDNA FLJ16445 fis, clone BRAMV3008937, highly similar
 to Metabotropic glutamate receptor 4 precursor.
 AK122836
 AK122836

VERSION
KEYWORDS
SOURCE
ORGANISM

AK122836.1 GI:34528033
Oligo capping; fis (full insert sequence).
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, M., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, S., Chiba, Y., Iehida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoshida, M., Houta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujii, Y., Kawabata, A., Hikiji, T., Kobatake, N., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039

TITLE

JOURNAL
PUBMED
REFERENCE
AUTHORS

Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakami, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 3850)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@ri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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AUTHORS
JOURNAL

Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakami, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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COMMENT

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FEATURES
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Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakami, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Location/Qualifiers
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US-10-828-332-7 (1-584) x AK122836 (1-3850)

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ACCESSION AR270511
VERSION AR270511.1 GI:29701745
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3884)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1074 31-DEC-2002;
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ACCESSION AR381464
VERSION AR381464.1 GI:40089522
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3884)
AUTHORS Chaudhari, N. and Roper, S.D.
TITLE Taste receptor for umami (monosodium glutamate) taste
JOURNAL Patent: US 6608176-A 14 19-AUG-2003;
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ORIGIN
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Score: 3004.50 Conservative: 6
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Best Local Similarity: 96.74% Indels: 1
Query Match: 96.70% Gaps: 1
DB: 6

US-10-828-332-7 (1-584) x AR381464 (1-3884)
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Job time : 7366 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2005, 17:59:49 ; Search time 178 Seconds
(without alignments)
1680.080 Million cell updates/sec

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Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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18	2052.5	66.1	877	1 MGR6 HUMAN	Q15303 homo sapien
19	2044	65.8	868	2 Q8G3I4	Q8g3i4 oryctolagus
20	2025	65.2	846	1 MGR6 RAT	P35349 rattus norv
21	1967.5	63.3	576	2 Q8CFQ7	Q8cfq7 mus musculu
22	1855	59.7	620	2 Q76E43	Q76e43 poephila gu
23	1813	58.4	977	2 Q9PWE1	Q9pwe1 ictalurus p
24	1284.5	41.3	1520	2 Q8NHA9	Q8nha9 homo sapien
25	1240.5	39.9	976	1 MGR DROME	P91685 drosophila
26	1223.5	39.4	780	2 Q7KQS9	Q7kqs9 drosophila
27	1223.5	39.4	1073	2 Q7QGQ8	Q7qgq8 drosophila
28	1223.5	39.4	1226	2 Q9V4U3	Q9v4u3 drosophila
29	1223.5	39.4	1264	2 Q9V4U4	Q9v4u4 drosophila
30	1181	38.0	933	2 Q75QW7	Q75qw7 apis mellif
31	1179	37.9	843	2 Q6S738	Q6s738 apis mellif

32	1171.5	37.7	872	1 MGR2 RAT	P31421 rattus norv
33	1155.5	37.2	877	1 MGR3 HUMAN	Q14832 mus sapien
34	1155.5	37.2	879	1 MGR3 MOUSE	Q9gyv82 mus musculu
35	1155.5	37.2	879	2 Q86YG6	Q86yg6 homo sapien
36	1152.5	37.1	879	1 MGR3 RAT	P31422 rattus norv
37	1150.5	37.0	872	1 MGR2 HUMAN	Q14416 homo sapien
38	1148.5	37.0	877	2 Q8TBH9	Q8tbh9 homo sapien
39	1148.5	37.0	1040	2 Q75QM6	Q75qm6 apis mellif
40	1129	36.3	1194	1 MGR1 HUMAN	Q13255 homo sapien
41	1122	36.1	1199	1 MGR1 RAT	P23385 rattus norv
42	1118.5	36.0	1156	2 Q98UC6	Q98uc6 gallus gall
43	1118	36.0	942	2 Q6J164	Q6j164 homo sapien
44	1118	36.0	1212	1 MGR5 HUMAN	P41594 homo sapien
45	1117	36.0	1188	2 Q98UC5	Q98uc5 gallus gall

ALIGNMENTS

RESULT 1

ID MGR4 RAT STANDARD; PRT; 912 AA.
AC P31423;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 4 precursor (mGluR4).
GN Name=Gm4; Synonyms=Gprc1d, Mglur4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=921110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93334699; PubMed=8338667;
RA O'Hara P.J., Sheppard P.O., Thøgersen H., Venezia D., Haldeman B.A.,
RT McGrane V., Houamed K.M., Thomsen C., Gilbert T.L., Mulvihill E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
RN [3]
RP INTERACTION WITH PRKCAP.
RX MEDLINE=20571397; PubMed=1122333;
RA El Far O., Airas J., Wischmeyer E., Nehring R.B., Karschin A.,
RT Betz H.;
RT "Interaction of the C-terminal tail region of the metabotropic
glutamate receptor 7 with the protein kinase C substrate PICK1.";
Eur. J. Neurosci. 12:4215-4221(2000).
CC -!- FUNCTION: Receptor for glutamate. The activity of this receptor is
mediated by a G-protein that inhibits adenylate cyclase activity.
CC -!- SUBUNIT: Interacts with PRKCAP.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Is widely distributed in the CNS. Predominant
expression is seen in the granule cells of the cerebellum.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; M92077; -; NOT_ANNOTATED_CDS.


```
Db 390 NRERIGQDSAYEQGKQVFVIDAVYAMGHAMHRLDCPRGVLCPRMDPVDGTQLLKY 449
Qy 122 IRNVNFGSIAGNPVTFNENGDAPEGYDIYQVLRNGSAEYKVIQSWTDHLHLRIEROMP 181
Db 450 IRNVNFGSIAGNPVTFNENGDAPEGYDIYQVLRNGSAEYKVIQSWTDHLHLRIEROMP 509
Qy 182 GSGQQLPRISICSLPCQGERKKTVMGMAACCHCEPCTGYQVDRYTCCTCPYDMRPTE 241
Db 510 GSGQQLPRISICSLPCQGERKKTVMGMAACCHCEPCTGYQVDRYTCCTCPYDMRPTE 569
Qy 242 RTSCQPIPIVKLEWDSPAWVLPFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 301
Db 570 RTSCQPIPIVKLEWDSPAWVLPFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 629
Qy 302 LAGIFLCVATTFLMTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
Db 630 LAGIFLCVATTFLMTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 689
Qy 362 APRFISPASQLAITFILISLQLLGCIVWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 421
Db 690 APRFISPASQLAITFILISLQLLGCIVWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 749
Qy 422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAFIPIFFGTS 481
Db 750 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAFIPIFFGTS 809
Qy 482 QSADKLYIQTTLTVSVLSASVSLSGLMYPKVYIIILFH 520
Db 810 QSADKLYIQTTLTVSVLSASVSLSGLMYPKVYIIILFH 548

RESULT 4
Q62MQ2
ID Q62MQ2 PRELIMINARY; PRT; 796 AA.
AC Q62MQ2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16766.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yanashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuna M., Murakawa K., Kanehori K., Takahashi-Pujii A., Oshima A.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131536; BAD18673.1; -.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0008067; F.metabotropic glutamate, GABA-B-like recepto. .; IEA.
DR GO; GO:0004872; E.receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mrglu_receptor.
DR InterPro; IPR001786; Mrglu_receptor4.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMRG.
DR PRINTS; PR01054; MTABOTROPICAR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_4; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 796 AA; 88492 MW; FAE466D1D45D3829 CRC64;
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Query Match 87.5%; Score 2719; DB 2; Length 796;

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Best Local Similarity 97.9%; Pred. No. 3e-213;
Matches 512; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy 62 NRERIGQDSAYEQGKQVFVIDAVYAMGHAMHRLDCPRGVLCPRMDPVDGTQLLKY 121
Db 274 DRERIGQDSAYEQGKQVFVIDAVYAMGHAMHRLDCPRGVLCPRMDPVDGTQLLKY 333
Qy 122 IRNVNFGSIAGNPVTFNENGDAPEGYDIYQVLRNGSAEYKVIQSWTDHLHLRIEROMP 181
Db 334 IRNVNFGSIAGNPVTFNENGDAPEGYDIYQVLRNGSAEYKVIQSWTDHLHLRIEROMP 393
Qy 182 GSGQQLPRISICSLPCQGERKKTVMGMAACCHCEPCTGYQVDRYTCCTCPYDMRPTE 241
Db 394 GSGQQLPRISICSLPCQGERKKTVMGMAACCHCEPCTGYQVDRYTCCTCPYDMRPTE 453
Qy 242 RTSCQPIPIVKLEWDSPAWVLPFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 301
Db 454 RTGCRPIPIIKLEWDSPAWVLPFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 513
Qy 302 LAGIFLCVATTFLMTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
Db 514 LAGIFLCVATTFLMTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 573
Qy 362 APRFISPASQLAITFILISLQLLGCIVWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 421
Db 574 APRFISPASQLAITFILISLQLLGCIVWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 633
Qy 422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAFIPIFFGTS 481
Db 634 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAFIPIFFGTS 693
Qy 482 QSADKLYIQTTLTVSVLSASVSLSGLMYPKVYIIILFHPEONVPKRRSLKAVVTAATM 541
Db 694 QSADKLYIQTTLTVSVLSASVSLSGLMYPKVYIIILFHPEONVPKRRSLKAVVTAATM 753
Qy 542 SNKFTQKGNFRPNGEAKSELLENLEPALATKQTYVYVYTNHAI 584
Db 754 SNKFTQKGNFRPNGEAKSELLENLEPALATKQTYVYVYTNHAI 796

RESULT 5
Q68EF4
ID Q68EF4 PRELIMINARY; PRT; 832 AA.
AC Q68EF4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
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Db 386 GLRIARDSSYEOGKVQVDAVYSMAVALHMHKELCPGYIGLCPRMVTIDGKELGY 445
Qy 122 IRNVFSGIAGNPVTNENGDAFGRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERMOWP 181
Db 446 IRANFNAGSAGTPTNENGDAFGRYDIYQYQINNKSTYKLIHWTNQLHLKVEDMOWA 505
Qy 182 GSGQOLPRISICSLPCQPGERKKTVMGACWCEPCTGYQYQVDRYTKCTCPYDMRPTEN 241
Db 506 NREHTHPASVCSLPCPKGERKKTVMGVPCCWCHCEGCEGYNQYQVDELSCCLPLDORPNIN 565
Qy 242 RTSQCPPIVTKLEWDSWPAVLPLFLAVGVIAATLVVVTVFVYNDTPIVVKASGRELSYVL 301
Db 566 RTGCQPIPIKLEWSPWAVPVFVAILGLIATTFVIVTVFVYNDTPIVVKASGRELSYVL 625
Qy 302 LAGIFLCYATTFILMAEPDLGTCSSRIIFGLGMSISYAALTKTNRIYRIPEQGRKSVS 361
Db 626 LTFGLFCYSITFLMAAPDTIICSPRIIFGLGMCFSYAALTKTNRIHRIPEQGRKSVT 685
Qy 362 APRFTSPASQALITFILISQLLGLICVWFVDPSPSHSVDFQDRTLDPRFARGVLKCDIS 421
Db 686 AKPFITSPASQALITFILISVQLLVFVWFVDPSPHPTIIDYGSQRTLDPENARGVLKCDIS 745
Qy 422 DLSLCLIGYSMLLMVTCVYAIKTRGVPEETENAKPIGFTWYTCIVWLAFIPFEGTS 481
Db 746 DLSLCLIGYSMLLMVTCVYAIKTRGVPEETENAKPIGFTWYTCIVWLAFIPFEGTS 805
Qy 482 QADKLYITQTTTLTVSVLSASVSGLMYPKVYIILFHPQNVKPKRKSXAVVTAATM 541
Db 806 QSAEKMYITQTTTLTVSMLSASVSGLMYPKVYIILFHPQNVKPKRKSXAVVTAATM 865
Qy 542 SNKFTQGNFRNGBAKSELNLETALATKOTVYVYTNHAI 584
Db 866 QSKLIQKGNDRNGEVKSELCSLETNTSSTTKTVISYNSHSI 908

RESULT 8
MGR8_RAT
ID MGR8_RAT STANDARD; PRT; 908 AA.
AC P0579;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 8 precursor (mGluR8).
GN Name=Gm8; Synonyms=Gprclh, Mglur8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97168760; PubMed=9016353;
RA Saugstad J.A., Kinzie J.M., Shinohara M.M., Segerson T.P.,
RA Westbrook G.L.;
RT "Cloning and expression of rat metabotropic glutamate receptor 8
RT reveals a distinct pharmacological profile.";
RL Mol. Pharmacol. 51:119-125(1997).
RN [2]
RP INTERACTION WITH PKCAPP.
RX MEDLINE=20571397; PubMed=11122333;
RA El Far O., Ahras J., Wischmeyer E., Nehring R.B., Karschin A.,
RA Betz H.;
RT "Interaction of the C-terminal tail region of the metabotropic
RT glutamate receptor 7 with the protein kinase C substrate PICK1.";
RL Eur. J. Neurosci. 12:4215-4221(2000).
CC -!- FUNCTION: Receptor for glutamate. The activity of this receptor is
CC mediated by a G-protein that inhibits adenylyl cyclase activity.
CC -!- SUBUNIT: Interacts with PKCAPP.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Prominent expression in olfactory bulb,
CC pontine gray, lateral reticular nucleus of the thalamus, and
CC piriform cortex. Less abundant expression in cerebral cortex,
CC hippocampus, cerebellum, and mamillary body.

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CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
Db HMBL; U63288; AAB09537.1; -.
Qy HSSP; P23385; LEW7.
Db RGD; 619858; Gm8.
Qy InterPro; IPR001828; ANF receptor.
Db InterPro; IPR00337; GPCR_Mgr.
Qy InterPro; IPR00162; Mglu_receptor.
Db InterPro; IPR00144; Mglu_receptor8.
Qy Pfam; PF00003; 7tm_3; 1.
Db Pfam; PF01094; ANF_receptor; 1.
Qy PRINTS; PR00248; GPCRMR.
Db PROSITE; PS00979; G-PROTEIN RECEPTOR F3_1; 1.
Qy PROSITE; PS00980; G-PROTEIN RECEPTOR F3_2; 1.
Db PROSITE; PS00981; G-PROTEIN RECEPTOR F3_3; 1.
Qy PROSITE; PS00982; G-PROTEIN RECEPTOR F3_4; 1.
Db PROSITE; PS00983; G-PROTEIN RECEPTOR F3_5; 1.
Qy G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
Db Signal; Transmembrane.
Qy SIGNAL 1 33 Potential.
Db CHAIN 34 908 Metabotropic glutamate receptor 8.
Qy DOMAIN 34 583 Extracellular (Potential).
Db TRANSMEM 584 608 1 (Potential).
Qy DOMAIN 609 620 Cytoplasmic (Potential).
Db TRANSMEM 621 641 2 (Potential).
Qy DOMAIN 642 647 Extracellular (Potential).
Db TRANSMEM 648 668 3 (Potential).
Qy DOMAIN 669 695 Cytoplasmic (Potential).
Db TRANSMEM 696 716 4 (Potential).
Qy DOMAIN 717 746 Extracellular (Potential).
Db TRANSMEM 747 768 5 (Potential).
Qy DOMAIN 769 781 Cytoplasmic (Potential).
Db TRANSMEM 782 803 6 (Potential).
Qy DOMAIN 804 818 Extracellular (Potential).
Db TRANSMEM 819 843 7 (Potential).
Qy DOMAIN 844 908 Cytoplasmic (Potential).
Db CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
Qy CARBOHYD 298 298 N-linked (GlcNAc...) (Potential).
Db CARBOHYD 452 452 N-linked (GlcNAc...) (Potential).
Qy CARBOHYD 480 480 N-linked (GlcNAc...) (Potential).
Db CARBOHYD 565 565 N-linked (GlcNAc...) (Potential).
Qy SEQUENCE 908 AA; 101866 MW; FCAB54CB8E3DD915 CRC64;
Db Query Match 76.3%; Score 2371; DB 1; Length 908;
Qy Best Local Similarity 74.8%; Pred. No. 9,7e-185;
Db Matches 436; Conservative 60; Mismatches 85; Indels 2; Gaps 2;
Qy 3 GVSSSLPRTMT-SGFDYFSSRTLDNRRNTWPAEFWEDNFCKLSRLAKGSHIKKCT 61
Db 327 GAVTILPKRASTIDGFDYFRSRTLANRRNVFAEFWEENFCCKLGSHG-KRNSHIKKCT 385
Qy 62 NREIGQDSAYEOGKVQVDAVYAMGHALHMHKELCPGVGLCPMDPVDGTOLKY 121
Db 386 GLRIARDSSYEQGKVQVDAVYSMAVALHMHKELCPGYIGLCPRMVTIDGKELGY 445
Qy 122 IRNVFSGIAGNPVTNENGDAFGRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERMOWP 181
Db 446 IRANFNAGSAGTPTNENGDAFGRYDIYQYQINNKSTYKLIHWTNQLHLKVEDMOWA 505
Qy 182 GSGQOLPRISICSLPCQPGERKKTVMGACWCEPCTGYQYQVDRYTKCTCPYDMRPTEN 241
Db 506 NREHTHPASVCSLPCPKGERKKTVMGVPCCWCHCEGCEGYNQYQVDELSCCLPLDORPNIN 565
Qy 242 RTSQCPPIVTKLEWDSWPAVLPLFLAVGVIAATLVVVTVFVYNDTPIVVKASGRELSYVL 301
Db 566 RTGCQPIPIKLEWSPWAVPVFVAILGLIATTFVIVTVFVYNDTPIVVKASGRELSYVL 625

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RESULT 11
Q68ED2
ID Q68ED2 PRELIMINARY; PRT; 915 AA.
AC Q68ED2;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Gm7 protein.
GN Name=Gm7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettner M.M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Trinchman J.W., Schmutz J., Dickson M.C.,
RA Rodriguez A.C., Goughwood J., Green J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080315; AAH0315.1; -.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mglu_receptor.
DR InterPro; IPR001883; Mglu_receptor7.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PRINTS; PR01057; MTABOTROPCTR.
DR PRINTS; PR00593; MTABOTROPCTR.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PROSITE; PS02059; G_PROTEIN_RECP_F3_4; 1.
SQ SEQUENCE 915 AA; 102218 MW; F0AF7AEDBFBCCF71 CRC64;

Query Match
Best Local Similarity 71.3%; Score 2214; DB 2; Length 915;
Matches 407; Conservative 75; Mismatches 100; Indels 2; Gaps 2;

Qy 3 GVSSSLPRMT-SGFDYFSSRTLDNNRRNTWPAEFWEDNFHCKLSRHALKKGSHIKCT 61
Db 332 GAITTPKRAIVEGFDAYFTSRTLENNRRNVFAEYWEENFNCKLTISGSKKEDTDRCCT 391
Qy 62 NREIGQDSAYEQEGKVQFDVAYMGCHALHAMHRLDCPGRVGLCPMDPVDGTOLIKY 121
Db 392 GQERIGKDSNYEQEGKVQFDVAYMAHALLHMKDLCAHYRGVCPMEQAGGKLLKY 451
Qy 122 IRNVNFSGIAGNPVTFNENGDAFGRYDIYQQLRN-GSAEYKVIGSWTDHLHLRIERMQW 180

452 IRNVNFSAGTVMFNKNGDAPGRYDIYQQLRNPGVRLIGQWTDLQLNIEDMQW 511
181 PGSQQLPRISCLPCOPGERKKTVMKMACWCEPCCTGYQYQVDRVTCCTCPYDMPTPE 240
512 KGVREIPPSVCTLPCKPGQKKTQKGTCCWTCPCDGYQYQDEMTQCHPCPYDQRPNE 571
241 NRTSCQPIVWLEWSDPAVLPLFLAVVGGIAATLFFVVVTFVRVYNDTPIVKASGRELSYV 300
572 NRTGCQNIPIKLEWSPWAVIPVFLAMGLIATIFWMAFIRVNDTPIVRASGRELSYV 631
301 LLAGIFLCYATTFMLIAEPDLGTCSLRRIIFLGMSISYAALLTKTNRIYRIFPGKRSV 360
632 LLTGIFLCYITTFMLIAKPDVAVCSFRFVLGLGMCISYAALLTKTNRIYRIFPGKRSV 691
361 SAPRFISPASQLAITFLISLILGICVWFVDPBSHVSVDQDQDRLDPRFARGLVKCDI 420
692 TAPRLISPTSQLAITSSLISVQLLVGFVFGVDPNIIIDYDEHKTNWPOARGVLKCDI 751
421 SDSLICLLGVSMMLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTTCIVMLAFIPFGT 480
752 TDLIQICSLGYSILLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTTCIVMLAFIPFGT 811
481 SQSADKLYIQTTTLTVSVLSASVSLGMLYMPKYIILFHPHQNVPRKRSGLKAVVTAAT 540
812 AQSAEKLYIQTTTLTISMLNSASVALGMLYMPKYIILFHPQLNVQKRKRSFKAIVTAAT 871
541 MSNKFTQKGFNPRNGEAKSCLNLETPALATKQTYTYTNHAI 584
872 MSRLSHKPSDRPNGEAKTELCENVDNPSPAKKYKVVYNNLVI 915

RESULT 12
MGR7_RAT
ID MGR7_RAT STANDARD; PRT; 915 AA.
AC P35400;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 7 precursor (mglur7).
GN Name=Gm7; Synonyms=Gprcig, Mglur7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=94117433; PubMed=8288585;
RA Okamoto N., Hori S., Akazawa C., Hayashi Y., Shigemoto R., Mizuno N.,
RA Nakanishi S.;
RT "Molecular characterization of a new metabotropic glutamate receptor
RT mglur7 coupled to inhibitory cyclic AMP signal transduction.";
RL J. Biol. Chem. 269:1231-1236(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Olfactory bulb;
RX MEDLINE=94195260; PubMed=8145723;
RA Saugstad J.A., Kinzie J.M., Mulvihill E.R., Segerson T.P.,
RA Westbrook G.L.;
RT "Cloning and expression of a new member of the L-2-amino-4-
RT phosphonobutyric acid-sensitive class of metabotropic glutamate
RT receptors.";
RL Mol. Pharmacol. 45:367-372(1994).
[3]
RN INTERACTION WITH PKCABP.
RP MEDLINE=20571397; PubMed=1122333;
RA El Far O., Airas J., Wischmeyer E., Nehring R.B., Karschin A.,
RA Betz H.;
RT "Interaction of the C-terminal tail region of the metabotropic
RT glutamate receptor 7 with the protein kinase C substrate PICK1.";
RL Eur. J. Neurosci. 12:4215-4221(2000).
CC -1- FUNCTION: Receptor for glutamate. The activity of this receptor is
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Job time : 182 secs

RA Schulz H.L., Stoeher H., Weber B.H.F.;
RT "Characterization of three novel isoforms of the metabotropic
RL glutamate receptor 7 (GRM7).";
RL Neurosci. Lett. 326:37-40(2002).
DR EMBL; AF458052; AAM47557.1; -.
DR HSSP; P23385; 1EWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto...; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mrglu_receptor.
DR InterPro; IPR001883; Mrglu_receptor7.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR07562; NCD3G; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PRINTS; PR01057; MTABOTROPCTR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 924 AA; 103375 MW; 32028B6156A71BFE CRC64;
Query Match 70.5%; Score 2189; DB 2; Length 924;
Best Local Similarity 70.8%; Pred. No. 7.4e-170;
Matches 401; Conservative 71; Mismatches 92; Indels 2; Gaps 2;
QY 3 GYSSSLPTMT-SGDRYFSSRTLNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKT 61
DB 332 GAITIQKRAIVEGFDAYFTSRTLENNRRNVFAEYWEENFCKLTISGSKKEDTDKCT 391
QY 62 NHERIGDSAYQEGKVQVIVDAVYANGHALHAMHDLCPGRVGLCPMDPVDGTQLLY 121
DB 392 GQERIGKDSNYEQEGKVQVIVDAVYAMAHALHMHKDLCADYRGVCPENEGAGGKLLKY 451
QY 122 IRNVNPSGIAGNPVTNENGDPGRYDIYQYQLRNGS-AEYKVIGSWTDHLHLRIERMOW 180
DB 452 IRNVNPSGAGTFVFNKNGDAPGRYDIYQYQTNTSNFGYRLIGQWTDDELQINIEDMOW 511
QY 181 PGSGQQLPRISICSLPQCPGKERKTKVGMACCMHCEPCTGYQYQVDRYTKCTCPYDMRPT 240
DB 512 GKGVRIPASVCTLPCKPGQRKTKGTCCWTCPCDGYQYQFDEMTQCHCPYDQRPNE 571
QY 241 NRTSQOPIPIVLEWSPWAVLPFLAVVGIATLFWVVTFRVNDTPIVKASGRELSYV 300
DB 572 NRTGCDIPIIKLEWSPWAVIPFLAVLGLIATIFVWATFIRYNDTPIVRASGRELSYV 631
QY 301 LLAGIFLCYATTFMTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSV 360
DB 632 LITGIFLCYITTFMTAKPDVAVCSFRRVFLGMCISYAALLTKTNRIYRIFEOGKRSV 691
QY 361 SAPRFISPASQLAITFILISLQLLGIQVWFVDPSPVDFQDQRTLDRFARGVLKCDI 420
DB 692 TAPRLISPTSQLAITSSLSVQLLGVFIWFGVDPNNIIDYDEHKTNPPEQARGVLKCDI 751
QY 421 SLSLILCLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIVWLAPIPIFFT 480
DB 752 TDLQIICSLGYSLLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIVWLAPIPIFFT 811
QY 481 SOSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPSONVPKRSLKAVVTAAT 540
DB 812 AQSAEKLYIQTTLTISMLSLASVALGMLYMPKVYIILFHPPELVQKRKRSKAVVTAAT 871
QY 541 MSNKFQKGNFRPNGEAKSELCELE 566
DB 872 MSRLSHKPSDRPNGEAKTELCEVND 897

Search completed: June 17, 2005, 18:17:24

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3050.5	98.2	912	2	JH0563	metabotropic gluta
2	2336	75.2	908	2	I49142	metabotropic gluta
3	2210	71.1	915	2	A49874	metabotropic gluta
4	2111.5	68.0	551	2	T30806	metabotropic gluta
5	2025	65.2	871	2	A46742	metabotropic gluta
6	1171.5	37.7	872	2	JH0561	metabotropic gluta
7	1155.5	37.2	879	2	JC7160	metabotropic gluta
8	1152.5	37.1	879	2	JH0562	metabotropic gluta
9	1123	36.1	1180	2	JC2132	metabotropic gluta
10	1122	36.1	1199	2	A41939	G protein-coupled
11	1118	36.0	1212	2	JC2131	metabotropic gluta
12	1117.5	36.0	1171	2	A42916	metabotropic gluta
13	1114.5	35.9	1218	2	S711376	glutamate receptor
14	989.5	31.8	999	2	T27628	hypothetical prote
15	871.5	28.0	1287	2	T21340	hypothetical prote
16	689.5	22.2	1078	2	F59362	calcium/polyvalent
17	678.5	21.8	1079	2	A56715	calcium receptor (
18	672.5	21.6	1095	2	S40476	Ca(2+)-sensing rec
19	666.5	21.5	1088	2	B56715	calcium receptor (
20	308.5	9.9	858	2	JC7683	taste receptor T1R
21	308	9.9	1099	2	T16283	hypothetical prote
22	212	6.8	960	2	JE0356	gamma-aminobutyric
23	133	4.3	402	2	T29703	hypothetical prote
24	118	3.8	814	2	JC7389	thyroid stimulating
25	115	3.7	721	2	AH3117	lp5a protein impo
26	112	3.6	414	2	B84600	hypothetical prote
27	107.5	3.5	808	2	T51138	probable glutamate
28	107	3.4	1034	2	AE3557	acriflavins resista
29	106.5	3.4	377	2	A69377	Na+/H+ antiporter

	Query Match	98.2%;	Score 3050.5;	DB 2;	Length 912;
	Best Local Similarity	98.6%;	Pred. No. 3.8e-241;		
	Matches 575;	Conservative	2;	Mismatches 5;	Indels 1; Gaps 1
Qy	3	GVSSSLPTRMT-SGFDRYFSRSLDNNRRNRIWFAEFMEDNFHCKLSRHALKKGSHIKKCT	61		
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Db	330	GAVTILPKRMSVRGDFRYFSRSLDNNRRNRIWFAEFMEDNFHCKLSRHALKKGSHIKKCT	389		
Qy	62	NRERIGODSAYBOEGKQVOFVIDAYVAMGHALHAMHRDLCPGRVGLCPRMPDVGDTQLLKY	121		
Db	390	NRERIGODSAYBOEGKQVOFVIDAYVAMGHALHAMHRDLCPGRVGLCPRMPDVGDTQLLKY	449		

Qy 122 IRNVFSGIAGNVTENEGDAPGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 181
Db 450 IRNVFSGIAGNVTENEGDAPGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 509
Qy 182 GSGQOLPRISCSLPCQPCGERKKTIVKGMACCHCEPCTGYQYQVDRYCTKTCPCYDMRPTE 241
Db 510 GSGQOLPRISCSLPCQPCGERKKTIVKGMACCHCEPCTGYQYQVDRYCTKTCPCYDMRPTE 569
Qy 242 RTSCQPIPIVLEWDSWPAVLPLFLAVVIGIAATLFFVVVTFVRVYNDTPIVKSASGRELSTVL 301
Db 570 RTSCQPIPIVLEWDSWPAVLPLFLAVVIGIAATLFFVVVTFVRVYNDTPIVKSASGRELSTVL 629
Qy 302 LAGIFLCVATTFMLTAEPDLGTCSSRLRIFLGLGMSISYAALLTKTNRIYRIFFEQGRKSVS 361
Db 630 LAGIFLCVATTFMLTAEPDLGTCSSRLRIFLGLGMSISYAALLTKTNRIYRIFFEQGRKSVS 689
Qy 362 APRFISPASQLAITFILISLQLLGICVWFVDPDSHVVDFQDQRTLDPFRFARGVVKCDIS 421
Db 690 APRFISPASQLAITFILISLQLLGICVWFVDPDSHVVDFQDQRTLDPFRFARGVVKCDIS 749
Qy 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPIFGTS 481
Db 750 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPIFGTS 809
Qy 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSILKAVVTAATM 541
Db 810 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSILKAVVTAATM 869
Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db 870 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 912
RESULT 2
149142
metabotropic glutamate receptor 8 - mouse
A:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49142
R:Duvoisin, R.M.; Zhang, C.; Ramonell, K.
J. Neurosci. 15, 3075-3083, 1995
A:Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb
A:Reference number: I49142; MUID:95233944; PMID:7722646
A:Accession: I49142
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-908 <RES>
A:Cross-references: UNIPROT:P47743; EMBL:U17252; NID:g854728; PIDN:AAA68149.1; PID:g8547
C:Genetics:
A:Gene: mGluR8
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor
Query Match 75.2%; Score 2336; DB 2; Length 908;
Best Local Similarity 74.1%; Pred. No. 9.9e-183; Mismatches 89; Indels 2; Gaps 2;
Matches 432; Conservative 60
Qy 3 GVSSSLPRMT-SGFDYFSSRTLDNNRNRIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 327 GAVTILPKRASIDGFDYFRSRTLANNRNWFAEFSGNGCKSGSHG-KRNSHIKKCT 385
Qy 62 NRERIGQDSAYEGEGKQVFDIVAYMGHALHAMHRLDCPGRVGLCPRMDDPVDGTQLLY 121
Db 386 GLERITARDSSYEQEGKQVFDIVAYSMAYALHNMHKLCPGYIGLCPRMVTIDGKELLY 445
Qy 122 IRNVFSGIAGNVTENEGDAPGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 181
Db 446 IRNVFSGIAGNVTENEGDAPGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 505
Qy 182 GSGQOLPRISCSLPCQPCGERKKTIVKGMACCHCEPCTGYQYQVDRYCTKTCPCYDMRPTE 241
Db 506 NREHTHPASVCSLPCQPCGERKKTIVKGVPCCHGRCGEGYNTQVDELSCLELCPDORPNIN 565

Qy 242 RTSCQPIPIVLEWDSWPAVLPLFLAVVIGIAATLFFVVVTFVRVYNDTPIVKSASGRELSTVL 301
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Db 626 LTGIFLCVATTFMLTAEPDLGTCSSRLRIFLGLGMSISYAALLTKTNRIYRIFFEQGRKSVS 685
Qy 362 APRFISPASQLAITFILISLQLLGICVWFVDPDSHVVDFQDQRTLDPFRFARGVVKCDIS 421
Db 686 APRFISPASQLAITFILISLQLLGICVWFVDPDSHVVDFQDQRTLDPFRFARGVVKCDIS 745
Qy 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPIFGTS 481
Db 746 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPIFGTS 805
Qy 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSILKAVVTAATM 541
Db 806 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSILKAVVTAATM 865
Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db 866 QSKLIQGNDRPNGEVKSSELSETNTSTKTITYSIDHSI 908
RESULT 3
A49874
metabotropic glutamate receptor 7 - rat
N:Alternate names: metabotropic glutamate receptor mGluR7
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: A49874; I57954
R:Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 269, 1231-1236, 1994
A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coupled to phospholipase C-beta2
A:Reference number: A49874; MUID:94117433; PMID:8288585
A:Accession: A49874
A:Status: preliminary; translated from GB/EMBL/DBDJ
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A:Cross-references: UNIPROT:P35400; GB:D16817; NID:g458728; PIDN:BAA04092.1; PID:g458729
R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L. Mol. Pharmacol. 45, 367-372, 1994
A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid receptor family
A:Reference number: I57954; MUID:94195260; PMID:8145723
A:Accession: I57954
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-915 <RES>
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A:Gene: mGluR7
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor
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Best Local Similarity 69.5%; Pred. No. 2e-172; Mismatches 100; Indels 2; Gaps 2;
Matches 406; Conservative 76
Qy 3 GVSSSLPRMT-SGFDYFSSRTLDNNRNRIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 332 GATIQPKRAIVGFDAYFTSRTLENNRNWFAEYWEENFNCKLTISGSKEDTDKCT 391
Qy 62 NRERIGQDSAYEGEGKQVFDIVAYMGHALHAMHRLDCPGRVGLCPRMDDPVDGTQLLY 121
Db 392 QGERIGKDSNVEQEGKQVFDIVAYMAHALHNMKOLCADYRGVCPCEMEQAGGKLLKY 451
Qy 122 IRNVFSGIAGNVTENEGDAPGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 180
Db 452 IRNVFSGIAGNVTENEGDAPGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 511
Qy 181 PGSSQQLPRISCSLPCQPCGERKKTIVKGMACCHCEPCTGYQYQVDRYCTKTCPCYDMRPTE 240

Db 512 GKGVEIPSSVCTLPCKPQQRKTKQGTCCCTCEPCDGYQFQDENTCQHCYPDORPNE 571
Qy 241 NRTSCQIPPIVLENDSPWAVLPFLAVVGIATFLVYVYVYNDTPIVKASGRELSTV 300
Db 572 NRTGQNIPIKLEWHSWAVIPVFLAMLGIATIPVMTATFIRYNDTPIVRASGRELSTV 631
Qy 301 LLAGIFLCVATTFELMAEADPLGTCSLRRIFLGLGHSISVAALLTKTNRIYRIFEOGRSV 360
Db 632 LTTGIFLCVYIITFLMAEDVAVCSFRFVFLGLGMCISVAALLTKTNRIYRIFEOGRSV 691
Qy 361 SAPRFTSPASQALAITFLISLQLLGICVWVVDPSHSVVDFOORTLDRPRARGVLKCDI 420
Db 692 TAPRLISPTSQALITSSLSVQLLGVIWFGVDDPNIIIDYDEHKTMNPEQARGVLKCDI 751
Qy 421 SDSLICLLGYMLLMVTCTVVAIKTRGVPEFNEAKPIGFTMYTTCIIVLAFIPIFFGT 480
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Qy 481 SOSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPBQNVPRKRSUKAVVTAAT 540
Db 812 AQSADKLYIQTTLTISMLNSASVALGMLYMPKVYIILFHPBQNVPRKRSUKAVVTAAT 871
Qy 541 MSNKFTQGNFRPNGEAKSELCELETALATKQTVVYTNHAI 584
Db 872 MSSRLSHKPSDRPNGEAKTELCELVDPNSPAKKYVSYNNLVI 915
RESULT 4
T30806
metabotropic glutamate receptor 7 - Fugu rubripes (fragment)
C:Species: Fugu rubripes
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T30806
R:Cottage, A.J.; Clark, M.; Hawker, K.; Umrانيا, Y.; Wheller, D.; Bishop, G.;
FEBS Lett. 443, 370-374, 1999
A:Title: Three receptor genes for plasminogen related growth factors in the genome of th
A:Reference number: Z20880; MUID:99148833; PMID:10025966
A:Accession: T30806
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <COT>
A:Cross-references: UNIPROT:Q9PWQ0; EMBL:AJ010317; NID:e1355235; PID:e1355236; PIDN:CAAC
C:Genetics:
A:Gene: GRM7
A>Note: intron positions not resolved (incomplete sequence)
C:Superfamily: metabotropic glutamate receptor 4
Query Match 68.0%; Score 2111.5; DB 2; Length 551;
Best Local Similarity 68.9%; Pred. No. 1.2e-164;
Matches 376; Conservative 82; Mismatches 87; Indels 1; Gaps 1;
Qy 16 PDYFSSRTLDNRRNIWFAEFWEDNFCKLSRHALKKGSHIKKTNRRIGQDSAYRQE 75
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Qy 76 GKQVVIDAVYAMGHAMHARDLCPGRVGLCPMDPDVDTQLLYIRNVNPSGAGNPV 135
Db 61 GKQVVIDAVYAMAHALSHMTHDLCFSGSGVCDKMDPVGEGRMLLYIHCYVNGSAGTCV 120
Qy 136 TPENGDAPGRYDIYQYQLRN-GSAEYKVGISWTDLHLRIERMOWPGSQQLPRISCSL 194
Db 121 MENEGDAPGRYDIYQYQMSNISNPGYRNIGQWTHLNLNLEMQSGGDRKIPESVCSF 180
Qy 195 PCQGERKTKVGMACCHCECTGTGYQVDRYCTCTCYDNRPENTRSCQPIVIPLE 254
Db 181 PCSEGERKTKVGMVPCCHCECTGTGYQVDRYCTCTCYDNRPENTRSCQPIVIPLE 240
Qy 255 WDSWAVLPFLAVVGIATFLVYVYVYNDTPIVKASGRELSTVLLAGIFLCVATTFPL 314
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Db 421 LMVTCVVAIKSRGVPEFNEAKPIGFTMYTTCIIVLAFIPIFFGTSGSADKLYIQTTL 480
Qy 495 TVSVLSASVSLGMLYMPKVYIILFHPBQNVPRKRSUKAVVTAATMSNKFQKGNFRN 554
Db 481 TVSMLSATVSLGMLYIIPKVYIILFHPBQNVPRKRSUKAVVTAATVTRLSQKSDKQN 540
Qy 555 GEAKSE 560
Db 541 GESKIE 546
RESULT 5
A46742
metabotropic glutamate receptor, mGluR6 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46742
R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi,
J. Biol. Chem. 268, 11868-11873, 1993
A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor
A:Reference number: A46742; MUID:93280152; PMID:8389366
A:Accession: A46742
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-871 <NA>
A:Cross-references: UNIPROT:P35349; GB:D13963; NID:G391856; PIDN:BAA03066.1; PID:G39185
A:Experimental source: retina
A>Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBI:133250)
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; transmembrane protein
Query Match 65.2%; Score 2025; DB 2; Length 871;
Best Local Similarity 68.6%; Pred. No. 2.5e-157;
Matches 371; Conservative 64; Mismatches 102; Indels 4; Gaps 2;
Qy 3 GVSSSLPRMT-SGPDYFSSRTLDNRRNIWFAEFWEDNFCKLSRHALKKGSHIKKCT 61
Db 319 GAITILPKRASIDGFDQYFMTSLNRRNIWFAEFWENFNCKLTSSGQSDSDSTRCT 378
Qy 62 NRERIGQDSAYEQQGKQVVIDAVYAMGHAMHARDLCPGRVGLCPMDPDVDTQLLY 121
Db 379 GEERIGQDSAYEQQGKQVVIDAVYAMGHAMHARDLCPGHTGLCPAMEPTDGRLLHY 438
Qy 122 IRNVNFSGIAGNPVTNENGDPGRYDIYQYQLRNGSAE---YKVGISWTHLHLRIERM 178
Db 439 IRNVNFSGIAGNPVTNENGDPGRYDIYQYQLRNGSAE---YKVGISWTHLHLRIERM 178
Qy 179 QWPGSQQLPRISCSLPCQGERKTKVGMACCHCECTGTGYQVDRYCTCTCYDMRP 238
Db 499 RWSGDPEHVPVPSQSLPCQGERKTKVGMVPCCHCECTGTGYQVDRYCTCTCYDMRP 558
Qy 239 TENRTSCQIPPIVLENDSPWAVLPFLAVVGIATFLVYVYVYNDTPIVKASGRELSTV 298
Db 559 TPNHTGCRPTPVRLTWSSPWAALPLLLAVLIGIMATTTIMATFMRHNDTPIVRASGRELSTV 618
Qy 299 YVLLAGIFLCVATTFELMAEADPLGTCSLRRIFLGLGHSISVAALLTKTNRIYRIFEOGR 358
Db 619 YVLLTGIFLCVATTFELMAEADPLGTCSLRRIFLGLGHSISVAALLTKTNRIYRIFEOGR 678
Qy 359 SVSAPRFTSPASQALAITFLISLQLLGICVWVVDPSHSVVDFOORTLDRPRARGVLK 418
Db 679 SVTPPPFISPTSQLITFLISLQVGVVIANLGAQPHSHVYDEQRTVDEQARGVLK 738
Qy 419 DISDSLICLLGYSMMLMVTCTVVAIKTRGVPEFNEAKPIGFTMYTTCIIVLAFIPIFF 478

Db 676 GAQRPKEIPSSQVFCIGLILVQIVMWSVWLIETPGT-----RRYTLPEKRETVILKC 730
QY 419 DISDLSLICLLGYSMMLAVTCTVYAIKTRGVPTNEAKPIGFTMYTTCIVWLAFIPIFF 478
Db 731 NVKSSMLISLTVDVVLVILCTVYAFKTRKCPENFEAKFIPTMYTTCIWLAFIPIFF 790
QY 479 GTSQADKLYIQTTTLTVSVLSASVSLGMLYMPKYIILFHPQNVPRKRSLSKAVTTA 538
Db 791 VTSSD---YRVQTTMCISVLSGFWVLGCLFAPKVHIVLFQPKN-----VVTH 837
QY 539 ATMSNKFTQKG 549
Db 838 RLHLNRFVSUG 848

RESULT 8
JH0562
metabotropic glutamate receptor 3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0562
R.Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002; PMID:1309849
A:Accession: JH0562
A:Molecule type: mRNA
A:Residues: 1-879 <TAN>
A:Cross-references: UNIPROT:P31422
A:Experimental source: brain
C:Comment: This protein is coupled to a G protein and evokes a variety of functions by
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
F:577-539/Domain: transmembrane #status predicted <TRI>
F:614-634/Domain: transmembrane #status predicted <TII>
F:646-664/Domain: transmembrane #status predicted <TII>
F:689-709/Domain: transmembrane #status predicted <TIV>
F:735-756/Domain: transmembrane #status predicted <TVI>
F:770-791/Domain: transmembrane #status predicted <TVI>
F:804-828/Domain: transmembrane #status predicted <VII>
F:209,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 37.1%; Score 1152.5; DB 2; Length 879;
Best Local Similarity 42.8%; Pred. No. 5.4e-86;
Matches 236; Conservative 84; Mismatches 196; Indels 35; Gaps 9;

QY 6 5SLPTMTSGDFRYSRTLDNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCTNR 65
Db 326 ASHPVRQ---FDYFQSLNPYNNRRNPWFDFWEQKFCSLQ---NKRNRQVCDKHLA 378
QY 66 ICQDSAYEKGKQVVIDAVYANGHALHAMHRDLCPGRVGLCPMPDPVDTQLLK-YIRN 124
Db 379 I-DSSNYEOKSIFVYNAVYAMAHAKMQRTLCPTNTTKLDCAMKILDGKLYKEYLLK 437
QY 125 VNFSGI-----AGNPVTNENGDA PRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERM 178
Db 438 INFTAPFNKGAADSLVKEITFDGGRYNNVNLQQTGGKSYLKVGHWAETLSLDVDSI 497
QY 179 QWPGSQQLPRSTICSLPCQGERKKTVMGMAWCHCEPCTGYQYQVDRYTCCTCPYDMRP 238
Db 498 HW--SRNSVPTSQCSDEPCAPNEMKNQPGDVCCWICIPCEPYEVLVDEFTCMDCGQWP 555
QY 239 TNRNRTSCQPIPIVKLEWDSFVAVLPLFVAVGIAATLFFVVTFRVNDTPIVKASGRELS 298
Db 556 TADLSGYNLPEDYIKWEDAWAIGPVTTIACLGFLCTCIVITVFIKHNTPLVKASGRELC 615
QY 299 YVLLAGIFLCYATTFELMIAEPDLGTCSLRIIFLGLGMSISYAALLTKTNRIYRIEQQGR 358
Db 616 YILLFGVSLSYCWTFFPIAKPSVICALRRLLGLTSFAICYALLTKTNRIADIGVKN 675

RESULT 9

JC2132

metabotropic glutamate receptor 5 A - human

C:Species: Homo sapiens (man)

C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996

C:Accession: JC2132

R.Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.

Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994

A:Title: Molecular cloning and the functional expression of two isoforms of human metab

A:Reference number: JC2131; MUID:94197696; PMID:7908515

A:Accession: JC2132

A:Molecule type: mRNA

A:Residues: 1-1180 <MIN>

C:Comment: This protein is coupled to guanine nucleotide binding proteins.

C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein

F:580-604/Domain: transmembrane #status predicted <TM1>

F:617-637/Domain: transmembrane #status predicted <TM2>

F:644-664/Domain: transmembrane #status predicted <TM3>

F:694-714/Domain: transmembrane #status predicted <TM4>

F:738-759/Domain: transmembrane #status predicted <TM5>

F:773-794/Domain: transmembrane #status predicted <TM6>

F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match

36.1%; Score 1123; DB 2; Length 1180;

Best Local Similarity 39.8%; Pred. No. 2e-83;

Matches 229; Conservative 111; Mismatches 198; Indels 38; Gaps 9;

QY 3 GVSSSLPTMTSGDFRYSRTLDNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCTN 62

Db 324 GITIKLQSPDVKWFDDYILKLRPETNHRNPWFQEFQHRFCRLGFPQENSKYNTKNS 383

QY 63 RERIGQDSAYEKGKQVVIDAVYANGHALHAMHRDLCPGRVGLCPMPDPVDTQLLKVI 122

Db 384 --SLTLKTHVQDSKMGFVINAISYMAVGLHNMQMSLCPGYAGLCDAMKPIDGRKLLES 441

QY 123 RVNFSGIAGNPVTNENGDA PRYDIYQY-QLRNGSAEYKVGISWTDHLHLRIERMQWP 181

Db 442 MKNFTGTGSGDITLFDENGDSGRYEIMNFKEGMDYFDYINVGSW-DNGELKMDDEW 500

QY 182 GSGQQLPRSTICSLPCQGERKKTVMGMAWCHCEPCTGYQYQVDRYTCCTCPYDMRPT 240

Db 501 SKKSNIIRSCVCEPEKQIKVIRKEVSCCTCTPCKENEYVDEYTCACKQLGSWPTD 560

QY 241 NRTSCQPIPIVKLEWDSFVAVLPLFVAVGIAATLFFVVTFRVNDTPIVKASGRELS 300

Db 561 DLTGCDLIPVQYLRWGDPEPIAAVVFACGLGLATLFTVTFVFIYRDTTPVKSRRCLYI 620

QY 301 LLAGIFLCYATTFELMIAEPDLGTCSLRIIFLGLGMSISYAALLTKTNRIYRIEQQGRSV 360

Db 621 ILAGICLGLYTCFLCIAKPKQYCYQLRIGIGLSFAMYSALVTKTNRITRIARLAGSKKI 680

QY 361 --SAPRFTSPASQLAITFILISLQLLGICVWFVDPSPSHVDFQDRTLDPRFARGVLKC 418

Db 681 CTKKRFNWSACQLVATILICIQIIVALFIMEPDDIMHDY-----PSIREVYLIC 733

QY 419 DISDLSLICLLGYSMMLAVTCTVYAIKTRGVPTNEAKPIGFTMYTTCIVWLAFIPIFF 478

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Db 734 NNTNLGVVTPGLGYNLLISCTFYAFKTRNVNPNANFNEAKYIAFTMTYTCIIWLAFAVPIYF 793
Qy 479 GTSQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVIILFHPQONVPRKSL----- 528
Db 794 GSN-----YKIITTCFASVLSATVALGCMFPVKVIILAKPERNVSFAFTTSTVVRMH 846
Qy 529 ---KRLKAVVTAATMSNKFQKGN----FRPNGEA 557
Db 847 VODGKSSSAARSSSLVNLWKRGRSGSETLRSNGKS 882

RESULT 10
A41939
G protein-coupled glutamate receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A41939; S15362
R/Houamed, K.M.; Kuifjper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill,
Science 252, 1318-1321, 1991
A/Title: Cloning, expression, and gene structure of a G protein-coupled glutamate receptor
A/Reference number: A41939; PMID:92022526; PMID:1658524
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Cross-references: UNIPROT:P23385; GB:M61099; NID:g397806; PIDN:AAAL9497.1; PID:g204460
A/Experimental source: cerebellum
A/Note: sequence extracted from NCBI backbone (NCBIP:60785)
R/Masu, M.; Tanabe, Y.; Tauchida, K.; Shigemoto, R.; Nakanishi, S.
Nature 349, 760-765, 1991
A/Title: Sequence and expression of a metabotropic glutamate receptor.
A/Reference number: S15362; PMID:91156047; PMID:1847995
A/Accession: S15362
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1199 <MAS>
A/Cross-references: EMBL:X57569; NID:g56646; PIDN:CAA40799.1; PID:g56647
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 36.1%; Score 1122; DB 2; Length 1199;
Best Local Similarity 38.9%; Pred. No. 2.4e-83;
Matches 239; Conservative 106; Mismatches 208; Indels 62; Gaps 12;

Qy 3 GVSSSLPTMTSGDPRYSSRTLDNNRNINWFAEFWEDNFHCKLSRHALKKGSHIKKCTN 62
Db 337 GITIKLQSPVQKWFDDYILKLRPETNRNPFQEFQHRFQCRLEGEPQENSKNKTCSN 396
Qy 63 RERIGQDSAYEQEGKQVVIDAVYAMGHALHAMHRDLCPRVGLCPRMDPVDGTQLLYI 122
Db 337 NESLEEN--YVQDSKMGFVINAIYMAHGLQNMHHALCPGHVGLCDAMKPIDGRKLLDPL 454
Qy 123 RNVNFSGIAGNPVTFNENGDAFGRIYDIQYQLRNGSA-EYKVGISWTDH-LHLRIERMQW 180
Db 455 IKSSFVGVSGEERWFDEKGDAPGRYDINLQYTEANRYDYVHVHGVTHGVLNIDDKYIOM 514
Qy 181 PEGSQQLPRSTCSLPQCGGERKKTVKG-MACCHCEPCTGYQYQVDRYTKCTCPYDMRPT 239
Db 515 NKSG--MVRVSCSEPCLGQIKVIRKGEVSCCWICTACKENEFVQDDEFTCRACDLGMPN 572
Qy 240 ENRTSCQPIPIVKLEWDSFWAVLPLFAVVGIAATLFVVVTFVRYNDTPIVKASGRELSY 299
Db 573 AELTQCEPIPVRYLEWSDIESIIAIFSLGILVTLFVTLFVLYRDTFPVVKSSRELCT 632
Qy 300 VLLAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRS 359
Db 633 IILAGIFLGYVCPFTLIAKPTTSCVQLRLLVGLSSAMCYSALVTKTNRARIILAGSKK 692
Qy 360 VSA---PRFISPASQALITFILISLQILGICVFWVVDPSHVSVDFOQRTLDPRFARGVLK 417
Db 693 ICTRKPFRMSAWAQVIAISILISVQLTLVVTLLIMEPPMILSY-----PSIKEVYLI 745
Qy 418 CDISLSLICLLGYSMLLMWTCVYAIKTRGVPETFNEAKPIGFTMTYTCIIWLAFAPIF 477
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Db 746 CNTSNLGNWAPVGVNGYLLINSCTFYAFKTRNVNPNANFNEAKYIAFTMTYTCIIWLAFAVPIY 805
Qy 478 FGTQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVIILFHPQONVPRKSL----- 532
Db 806 FGSN-----YKIITTCFASVLSATVALGCMFPVKVIILAKPERNV-----RSAFTTSD 854
Qy 533 -----KAVVTAATMSNKFQKGN----GNFRNGEAKS-----ELC 562
Db 855 VVRMHVGDGKLPCHRSNTFLNIFRKRKPGAGNANSNGKSVSWSEPGGRQAPKGQHVWQRLS 914
Qy 563 ENLETPALATKQTYV 577
Db 915 VHVKTNETACNQTA 929

RESULT 11
JC2131
metabotropic glutamate receptor 5 B - human
C/Species: Homo sapiens (man)
C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C/Accession: JC2131
R/Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A/Title: Molecular cloning and the functional expression of two isoforms of human metabo
A/Reference number: JC2131; PMID:94197696; PMID:7908515
A/Accession: JC2131
A/Molecule type: mRNA
A/Residues: 1-1212 <MIN>
C/Comment: This protein is coupled to guanine nucleotide binding proteins.
C/Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
F:580-604/Domain: transmembrane #status predicted <TM1>
F:617-637/Domain: transmembrane #status predicted <TM2>
F:644-664/Domain: transmembrane #status predicted <TM3>
F:694-714/Domain: transmembrane #status predicted <TM4>
F:738-759/Domain: transmembrane #status predicted <TM5>
F:773-794/Domain: transmembrane #status predicted <TM6>
F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 36.0%; Score 1118; DB 2; Length 1212;
Best Local Similarity 39.4%; Pred. No. 5.2e-83;
Matches 231; Conservative 111; Mismatches 197; Indels 48; Gaps 10;

Qy 3 GVSSSLPTMTSGDPRYSSRTLDNNRNINWFAEFWEDNFHCKLSRHALKKGSHIKKCTN 62
Db 324 GITIKLQSPVQKWFDDYILKLRPETNRNPFQEFQHRFQCRLEGEPQENSKNKTCSN 383
Qy 63 RERIGQDSAYEQEGKQVVIDAVYAMGHALHAMHRDLCPRVGLCPRMDPVDGTQLLYI 122
Db 384 --SILTAKTHVQDSKMGFVINAIYSMAVGLHNMQMSLCPGVAGLCDAMKPIDGRKLLSL 441
Qy 123 RNVNFSGIAGNPVTFNENGDAFGRIYDIQYQLRNGSAEYKVGISWTDHHLRIERMQWP 181
Db 442 MKTNFTGVSQDTILFDENGSDSPGRYEIMNFKMGKQYFDYINVGSW-DNGELKMDDDDEV 500
Qy 182 GSGQQLPRSTCSLPQCGGERKKTVKG-MACCHCEPCTGYQYQVDRYTKCTCPYDMRPT 240
Db 501 SKSNIIIRVSCSEPCGQIKVIRKGEVSCCWTCTPKENYVDFETCTKACQIGSWPTD 560
Qy 241 NRTSCQPIPIVKLEWDSFWAVLPLFAVVGIAATLFVVVTFVRYNDTPIVKASGRELSY 300
Db 561 DLTGCDLIPVQLRWGDPEPIAAVFAVACLGALLATLFVTVVFIYRDTFPVVKSSRELCT 620
Qy 301 VLLAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRS 360
Db 621 ILAGICLGYLCTFCLIAKPKQIYCYLQRIIGLSPAMSYSALVTKTNRARIILAGSKKI 680
Qy 361 --SAPRISPASQALITFILISLQILGICVFWVVDPSHVSVDFOQRTLDPRFARGVLK 418
Db 681 CTKPRFMSACAVJUIAFILICIGIIVAFINPEPDMIDY-----PSIREVYLIC 733
Qy 419 DISDLSLICLLGYSMLLMWTCVYAIKTRGVPETFNEAKPIGFTMTYTCIIWLAFAPIF 478
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hypothetical protein ZC506.4 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T27628
R/Harris, B.
submitted to the EMBL Data Library, December 1994
A/Reference number: Z20395
A/Accession: T27628
A/Status: preliminary; translated from GB/EMBL/DDDBJ
A/Molecule type: DNA
A/Residues: 1-999 <Wtl>
A/Cross-references: UNIPROT:Q09630; EMBL:Z47073; PIDN:CAA87374.1; GSPDB:GNO0028; CESP:ZC506.4
A/Experimental source: clone ZC506
C/Genetics:
A/Gene: CESP:ZC506.4
A/Map position: X
A/Introns: 32/2; 65/3; 77/3; 113/2; 140/3; 177/2; 240/2; 277/1; 315/2; 439/2; 471/3; 591/2
C/Superfamily: metabotropic glutamate receptor 4

Query Match	31.8%;	Score	989.5;	DB 2;	Length	999;
Best Local Similarity	35.9%;	Pred. No.	1.3e-72;			
Matches	223;	Conservative	102;	Mismatches	211;	Indels
						85; Gaps
						17;
Qy	8	LPTMTSGFDRYFSS--RTLDNNRRNTWFAEFWEDNFHCKLSRHALKKGSHIKKCTNRER	65			
Db	389	LASQKVSFEYFNSLHPGTEAFERNKWLRELQVKYKCEFD---TPPGSTASRC---ED	442			
Qy	66	IGQDS-AYEQEGKQVFVIDAVYANGHALHAMRDLCG-----RVGLCPMD	111			
Db	443	IKOSTEGNADDKQVFVIDAVYAIHAHGLQSMQAICPDDAIENHWISRYSKQPEICHAMQ	502			
Qy	112	PVDGTQLLK-YIRNVNFSG-----IAGNPVTFNENGDAFGRYDIYQYL	154			
Db	503	NIDGSDFYQYLLKVNFTGKTIISFSSFRLSPPFSDIVGKFRFSPQGDGPASTILTYKP	562			
Qy	155	R-----NGSAEYKVGISWTDLHLRIERMOWPGSGQOLPRISICSLPQCPGERK	202			
Db	563	KSMDKRRMTDDDESSPDYVEIGHWSENNTIYEKNLW-WDPDHTPVSVCSLPCCKIGFRK	621			
Qy	203	KTVKGMACCHCECTCQYQVDRYTKCTCPYDMRPTENRTSCQPIPIVKLE---WDSWP	259			
Db	622	QLIKDEQCCWACSKCEDYEYLINETHCVGCEQHWPTKDRKGCPDLSLQKYWRWSMY	681			
Qy	260	AVLPLFLAVGVIAATLFWVTVFRYNDTPIVKASGRELSVLLAGIFLCYATTFLMIAEP	319			
Db	682	SLVPTILAVFGIIATLFIWVVIYNETPVVKASGRELSYILLTSMIMCYMTFVLLSKP	741			
Qy	320	DLGTCSERRFLPLGMSISYAAALTKNRIYRIEQGKRSVSAPRFTSPASOLAITILI	379			
Db	742	SAIVCAIKRTGIGTIGFAFSLYSAMPVKNRIFRIF--STRSAQRPRFISPISQVVMATLA	799			
Qy	380	SLQLLGICVWFVPDPSHVVDFQQRTLDRFARGVLKCDISLDSLCLIGYSMLLMVTC	439			
Db	800	GVQLIGSLIWLVSVP-----PGWRHHYPTRDQVLTLCNVPDHHFLYSLAYDGFLLVC	852			
Qy	440	TVYAIKTRGVPEETNEAKPIGFTMYTTCIVWLAFIPIPFGTSGQADKLIYQTTLTVSVS	499			
Db	853	TTVAVKTRKVPENFNETKFIQFSMYTTCVWMLSIFFFFGTGS---FOIQTSLSLCISIS	909			
Qy	500	LSASVSLGMLYMPKVVYILLHPENQVPRKESLKVAVTAAATMSNKKFTQGNFRPNGEAKS	559			
Db	910	MSANVALACIYFPKMLIILFEKKNVRKQE-----GESMLNK-----SSRSLGNCSS	956			
Qy	560	ELCEN-LETP-----ALATKQT	575			
Db	957	RLCANSIDEPNOYTALLTDS	977			

C;Accession: T21340; T22252
F;McMurray, A.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19409
A;Accession: T21340
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1267<WIL>
A;Cross-references: UNIPROT:Q93564; EMBL:Z78418; PIDN: CAB01699.1; GSPDB:GN00019; CESP:F45H11.4
A;Experimental source: clone F25D7
R;Kelly, P.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19537
A;Accession: T22252
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1267<WII>
A;Cross-references: EMBL:Z78420; PIDN: CAB01711.1; GSPDB:GN00019; CESP:F45H11.4
A;Experimental source: clone F45H11
C;Genetics:
A;Gene: CESP:F45H11.4
A;Map position: 1
A;Introns: 38/3; 90/2; 149/3; 207/1; 356/2; 413/2; 458/2; 520/3; 691/3; 777/2; 796/2; 899/2

Query Match 28.08; Score 871.5; DB 2; Length 1267;
Best Local Similarity 35.38; Pred. No. 7.8e-63;
Matches 193; Conservative 100; Mismatches 196; Indels 57; Gaps 13;

Qy 15 GFDYFSSRTLDNNRNINFAEFWEDNFHCKLS - RHALKKGSHIKKTNRRIGQDSAYE 73
Db 328 GFRQYYTALHPENNTMNPWFREFWQKQCPAVSKEDKNENIRICSGDENL--DEQYK 385
Qy 74 QEGKVQVIVDAVYAMGHALHAMRDLCPRVGLCPRMDPVDGTCQLLKXIRNVNPFSGIAGN 133
Db 386 EDPKLSQVINSIRVALGLKAMTQDRCDNSTLCTEMLSRNGTLLYELLNVTSYDQFKQ 445
Qy 134 PVTFNENGDPGRYDIQY----QLRNGSAEYKVIQVSTDHLRLRERMQPGSG----- 184
Db 446 PVTFDRNGDPNAVYDILNYIGTKOLDN---PYNEVGSFKSINDYGYVEELDMTAKSMFFDK 502
Qy 185 -QQLPRSICSLPCQGERKKTIVKGMACCHCEPCTGYQYQVDRYT--CKTCTPYDMRPTEN 241
Db 503 TELLPSVCSRPCGIGQRQ--ETMACCMICESCLODIQ--VNKTNQCMNCTLGSWPNAN 559
Qy 242 RTSQPTPIVKLEWDSWPAVLPLFVAVVGTAAATLFFVVVTFVRVYNDTPIVKASGRELSYVL 301
Db 560 RTGCEYIPEVSWTSFEGHIALVAVTGITSMATLAVFLRHNSTPVPVKSITRELSYII 619
Qy 302 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFBQGRKSV- 360
Db 620 LSGLVACYAVSFALLATPSTTSCTFIRVPIAFVAVYSALLTKTNRIARILAGSKKRIL 679
Qy 361 -SAPRPTSPASQAIAITFILSLQLLGICVWFVVD--PSHSVVDQDQRTLDPRFARGVLKC 418
Db 680 TKPRFLTTFISQVVITWILVAVQCVIVGVGLMRDWPDATYAKYALPKL-----ILEC 732
Qy 419 DISDLSLICLLGYSMLLVMTCTVYAIKTRGVPTENEAKDIGFTM----- 463
Db 733 DTETKSFILPFFWDFFLITLCTLYAFKTRMLPENFNEAKFIGFTISQPAKSLPFFQKEHV 792
Qy 464 ----YTTCTIVMLAPIPIFFGTGSADKLYQTITTLTVSVLSLSASVSIGMLYMPKVIILF 519
Db 793 IIFQYCTIVVWVIAFLVLMGTHTKA-----LVMSFSYLSASVALALLFFPKLYIILM 845
Qy 520 HPEQNV 525
Db 846 HPEKNI 851

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2005, 18:07:59 ; Search time 47 Seconds
(without alignments)
927.554 Million cell updates/sec

Title: US-10-828-332-7
Perfect score: 3107
Sequence: 1 MPGVSSSLPRTMTSGDRYF.....LETPALATKQTVVYVTHAI 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
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- 5: /cgn2_6/ptodata/1/1aa/PTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3050.5	98.2	604	US-09-820-809-13	Sequence 13, Appli
2	3050.5	98.2	912	PCT-US91-09422-19	Sequence 19, Appli
3	3004.5	96.7	912	US-08-617-785-2	Sequence 2, Appli
4	3004.5	96.7	912	US-09-641-318-2	Sequence 2, Appli
5	3004.5	96.7	912	US-09-817-464-2	Sequence 2, Appli
6	2370	76.3	908	US-08-855-146-2	Sequence 2, Appli
7	2328	74.9	908	US-08-823-110-1	Sequence 1, Appli
8	2328	74.9	908	US-08-604-298-1	Sequence 1, Appli
9	2219	71.4	915	US-08-617-785-12	Sequence 12, Appli
10	2219	71.4	915	US-09-817-464-12	Sequence 12, Appli
11	2210	71.1	915	US-08-453-862-2	Sequence 2, Appli
12	2210	71.1	915	US-08-452-734A-2	Sequence 2, Appli
13	2210	71.1	915	US-08-176-401B-2	Sequence 2, Appli
14	2210	71.1	915	PCT-US94-14989-2	Sequence 2, Appli
15	2191.5	70.5	867	US-08-617-785-4	Sequence 4, Appli
16	2191.5	70.5	867	US-09-817-464-4	Sequence 4, Appli
17	2191.5	70.5	922	US-08-617-785-14	Sequence 14, Appli
18	2191.5	70.5	922	US-09-817-464-14	Sequence 14, Appli
19	2052.5	66.1	877	US-08-407-875-2	Sequence 2, Appli
20	2052.5	66.1	877	US-09-277-858-2	Sequence 2, Appli
21	2040.5	65.7	877	US-09-126-280-2	Sequence 2, Appli
22	1861.5	59.9	481	US-08-617-785-8	Sequence 8, Appli
23	1861.5	59.9	481	US-09-817-464-8	Sequence 8, Appli
24	1172.5	37.7	872	US-08-337-797A-2	Sequence 2, Appli
25	1172.5	37.7	872	US-09-258-523-2	Sequence 2, Appli
26	1155.5	37.2	879	US-08-794-158-2	Sequence 2, Appli
27	1148.5	37.0	879	US-08-072-574-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-820-809-13
; Sequence 13, Application US/09820809
; Patent No. 6608176
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARI, NIRUPA
; APPLICANT: ROBER, STEPHEN D.
; TITLE OF INVENTION: TASTE RECEPTOR FOR UMAMI (MONOSODIUM GLUTAMATE) TASTE
; FILE REFERENCE: 70373/275576
; CURRENT APPLICATION NUMBER: US/09/820,809
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,454
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-820-809-13

Query Match	98.2%	Score 3050.5;	DB 4;	Length 604;
Best Local Similarity	98.6%	Pred. No. 2.7e-300;		
Matches	575;	Conservative	2;	Mismatches 5; Indels 1; Gaps 1;
QY	3	GVSSSLPRTMT-SGPDYFSSRTLDNNRRNIWFAPFWEDNFHCKLSRHALKKGSHIKKCT	61	
Db	22	GAVTTLPRKMSVRGPDYFSSRTLDNNRRNIWFAPFWEDNFHCKLSRHALKKGSHIKKCT	81	
QY	62	NRERIGDSAYEKGKQVFIDAVYAMGHALHMHARDLCPGRVGLCPRMDPVDGTQLLKY	121	
Db	82	NRERIGDSAYEKGKQVFIDAVYAMGHALHMHARDLCPGRVGLCPRMDPVDGTQLLKY	141	
QY	122	IRNVNFGSIAGNPVTFFNENGDPAGRYDIYQQLRNGSAEYKVGISWTDLHLRIERMQWP	181	
Db	142	IRNVNFGSIAGNPVTFFNENGDPAGRYDIYQQLRNGSAEYKVGISWTDLHLRIERMQWP	201	
QY	182	SGGQOLPRISICSLPCQGERKKTVMKMACCHCEPCTGYQYQVDRYTKCTCYDMRPTEN	241	
Db	202	SGGQOLPRISICSLPCQGERKKTVMKMACCHCEPCTGYQYQVDRYTKCTCYDMRPTEN	261	
QY	242	RTSCOPIPIVKLEWDSFWAVLPLFVAVVGIATLFWVTVFYNDTPVVKASGRELSSYL	301	
Db	262	RTSCOPIPIVKLEWDSFWAVLPLFVAVVGIATLFWVTVFYNDTPVVKASGRELSSYL	321	
QY	302	LAGIFLCVATTFMLAEPLDGTCSLRRIFLGLGMSISYAALITKTNRIYRIFEQGKRSVS	361	
Db	322	LAGIFLCVATTFMLAEPLDGTCSLRRIFLGLGMSISYAALITKTNRIYRIFEQGKRSVS	381	
QY	362	APRFTSPASQLAITFILISLQLLGCVMFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS	421	

Db 382 APRFISPAQLAITFILISLQLLGICVWVDPSPSHVDFDQRTLDPRFARGVLKCDIS 441
Qy 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPFPGTS 481
Db 442 DLSLICLLGYSMMLMVTCTVVAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPFPGTS 501
Qy 482 QSAKLYIQTTLTIVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSLSKAVVTAATM 541
Db 502 QSAKLYIQTTLTIVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSLSKAVVTAATM 561
Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYVYTNHAI 584
Db 562 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYVYTNHAI 604

RESULT 2

PCT-US91-09422-19
; Sequence 19, Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481
; FILING DATE: 30-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/626,806
; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-6PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-09422-19

Query Match 98.2%; Score 3050.5; DB 5; Length 912;
Best Local Similarity 98.6%; Pred. No. 5.2e-300;
Matches 575; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
Qy 3 GVSSSLPRTMT-SGFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKCT 61
Db 330 GAVTILPKRMSVGRGFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKCT 389

Qy 62 NRERIGODSAYEGBGVQFVIDAVYAMGHALHAMHRLDCPRVGLCPMPDPDVGDTQLLKY 121
Db 390 NRERIGODSAYEGBGVQFVIDAVYAMGHALHAMHRLDCPRVGLCPMPDPDVGDTQLLKY 449
Qy 122 IRNVFSGIAGNPVTNENGDAFGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERQWMP 181
Db 450 IRNVFSGIAGNPVTNENGDAFGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERQWMP 509
Qy 182 GSGOQLPRSTCSLPQGBERKTKVGNACCMHCEPCTGYOYVDRTYTKCTCPYDMRPTEN 241
Db 510 GSGOQLPRSTCSLPQGBERKTKVGNACCMHCEPCTGYOYVDRTYTKCTCPYDMRPTEN 569
Qy 242 RTSCQPIPIVKLEWDSWAVLPLFLAVVGLAATLFFVVVTFVRYNDTPIVKASGRELSVVL 301
Db 570 RTSCQPIPIVKLEWDSWAVLPLFLAVVGLAATLFFVVVTFVRYNDTPIVKASGRELSVVL 629
Qy 302 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEGQKRSVS 361
Db 630 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEGQKRSVS 689
Qy 362 APRFISPAQLAITFILISLQLLGICVWVDPSPSHVDFDQRTLDPRFARGVLKCDIS 421
Db 690 APRFISPAQLAITFILISLQLLGICVWVDPSPSHVDFDQRTLDPRFARGVLKCDIS 749
Qy 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPFPGTS 481
Db 750 DLSLICLLGYSMMLMVTCTVVAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPFPGTS 809
Qy 482 QSAKLYIQTTLTIVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSLSKAVVTAATM 541
Db 810 QSAKLYIQTTLTIVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSLSKAVVTAATM 869
Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYVYTNHAI 584
Db 870 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYVYTNHAI 912

RESULT 3

US-08-617-785-2
; Sequence 2, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Putner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-2

Query Match 96.7%; Score 3004.5; DB 3; Length 912;
Best Local Similarity 96.7%; Pred. No. 2.4e-295;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
Qy 3 GVSSSLPRTMT-SGFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKCT 61
Db 330 GAVTILPKRMSVGRGFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKCT 389

Db 330 GAVTILPKRMSVRGFDYFSSRTLDNNRRNTWPAEFWEDNFCKLSRHALKKGSHVKKCT 389
Qy 62 NRERIGQDSAYEQEGKQVQFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLLKY 121
Db 390 NRERIGQDSAYEQEGKQVQFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLLKY 449
Qy 122 IRNVNFSGIAGNPTVFENGDAPGRYDIYQQLRNGSAEYKVIKGSWTDLHLRIERMOWP 181
Db 450 IRNVNFSGIAGNPTVFENGDAPGRYDIYQQLRNGSAEYKVIKGSWTDLHLRIERMOWP 509
Qy 182 GSGQQLPRISICSLPCQGERKKTVMKMACCHCEPCTGYQVQVDRYCTCTCPYDMRPTEN 241
Db 510 GSGQQLPRISICSLPCQGERKKTVMKMACCHCEPCTGYQVQVDRYCTCTCPYDMRPTEN 569
Qy 242 RTSQOPIPIVKLEWDSWAVLPLFLAVVGIATLFFVVTTFVRYNDTPIVKASGRELSYVL 301
Db 570 RTGCRPIPIKLEWDSWAVLPLFLAVVGIATLFFVVTTFVRYNDTPIVKASGRELSYVL 629
Qy 302 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
Db 630 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 689
Qy 362 APRFISPASQLAITFILISLQLLGCVMFVVDPSHVVDFODORTLDPFRFARGVLKCDIS 421
Db 690 APRFISPASQLAITFILISLQLLGCVMFVVDPSHVVDFODORTLDPFRFARGVLKCDIS 749
Qy 422 DLSLICLLGYSMLLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTCIIVWLAFIPIFFGTS 481
Db 750 DLSLICLLGYSMLLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTCIIVWLAFIPIFFGTS 809
Qy 482 QSAOKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPKRSKAVVTAATM 541
Db 870 SNKFTQKGNFRPNGEAKSELCELENLEAPALATKQTYVTVYTNHAI 912

RESULT 4
US-09-641-318-2
; Sequence 2, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; WU, SU
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELI LILLY AND COMPANY
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: INDIANA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,318
; FILING DATE: 18-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,178A
; FILING DATE: 12-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: GAYLO, PAUL J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10579
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756

TELEX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-641-318-2

Query Match
Best Local Similarity 96.7%; Score 3004.5; DB 3; Length 912;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
Qy 3 GVSSSLPFRMT-SGFDYFSSRTLDNNRRNTWPAEFWEDNFCKLSRHALKKGSHVKKCT 61
Db 330 GAVTILPKRMSVRGFDYFSSRTLDNNRRNTWPAEFWEDNFCKLSRHALKKGSHVKKCT 389
Qy 62 NRERIGQDSAYEQEGKQVQFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLLKY 121
Db 390 NRERIGQDSAYEQEGKQVQFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLLKY 449
Qy 122 IRNVNFSGIAGNPTVFENGDAPGRYDIYQQLRNGSAEYKVIKGSWTDLHLRIERMOWP 181
Db 450 IRNVNFSGIAGNPTVFENGDAPGRYDIYQQLRNGSAEYKVIKGSWTDLHLRIERMOWP 509
Qy 182 GSGQQLPRISICSLPCQGERKKTVMKMACCHCEPCTGYQVQVDRYCTCTCPYDMRPTEN 241
Db 510 GSGQQLPRISICSLPCQGERKKTVMKMACCHCEPCTGYQVQVDRYCTCTCPYDMRPTEN 569
Qy 242 RTSQOPIPIVKLEWDSWAVLPLFLAVVGIATLFFVVTTFVRYNDTPIVKASGRELSYVL 301
Db 570 RTGCRPIPIKLEWDSWAVLPLFLAVVGIATLFFVVTTFVRYNDTPIVKASGRELSYVL 629
Qy 302 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
Db 630 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 689
Qy 362 APRFISPASQLAITFILISLQLLGCVMFVVDPSHVVDFODORTLDPFRFARGVLKCDIS 421
Db 690 APRFISPASQLAITFILISLQLLGCVMFVVDPSHVVDFODORTLDPFRFARGVLKCDIS 749
Qy 422 DLSLICLLGYSMLLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTCIIVWLAFIPIFFGTS 481
Db 750 DLSLICLLGYSMLLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTCIIVWLAFIPIFFGTS 809
Qy 482 QSAOKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPKRSKAVVTAATM 541
Db 810 QSAOKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPKRSKAVVTAATM 869
Qy 542 SNKFTQKGNFRPNGEAKSELCELENLEAPALATKQTYVTVYTNHAI 584
Db 870 SNKFTQKGNFRPNGEAKSELCELENLEAPALATKQTYVTVYTNHAI 912

RESULT 5
US-09-817-464-2
; Sequence 2, Application US/09817464
; Patent No. 6515107
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILING DATE: 12-MAR-1997
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/09/817,464
; CURRENT FILING DATE: 2001-03-26
; EARLIER APPLICATION NUMBER: US/08/617,785
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7

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; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-464-2

Query Match          96.7%; Score 3004.5; DB 4; Length 912;
Best Local Similarity 96.7%; Pred. No. 2.4e-295;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

Qy  3 GVSSSLPRTMT-SGFDRYFSSRTLDNNRNWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db  330 GAVTILPKRMSVRGDFRYFSSRTLDNNRNWFAEFWEDNFHCKLSRHALKKGSHVKKCT 389

Qy  62 NRERIGDSAYEQGKQVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLKY 121
Db  390 NRERIGDSAYEQGKQVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLKY 449

Qy  122 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERQWP 181
Db  450 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERQWP 509

Qy  182 GSGQOLPRISCSLPCQGERKKTVMGMAACWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 241
Db  510 GSGQOLPRISCSLPCQGERKKTVMGMPCCWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 569

Qy  242 RTSQOPIPIVKLEWDSWAVLPLFVAVVGIATLTVVVTFRVYNDTPIVKASGRELSYVL 301
Db  570 RTGCRPIPIIKLEWDSWAVLPLFVAVVGIATLTVVVTFRVYNDTPIVKASGRELSYVL 629

Qy  302 LAGIFLCYATFLMIABPDLTGCSLRIRIFLGLGMSISYAALLTKTNRIYRIFEQKRSVS 361
Db  630 LAGIFLCYATFLMIABPDLTGCSLRIRIFLGLGMSISYAALLTKTNRIYRIFEQKRSVS 689

Qy  362 APRISPASOLAITFILISLQLLGCIVFWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 421
Db  690 APRISPASOLAITFILISLQLLGCIVFWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 749

Qy  422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPETFEAKPIGFTMYTTCIWLAFIPIFFGTS 481
Db  750 DLSLICLLGYSMMLMVTCTVYAIKTRGVPETFEAKPIGFTMYTTCIWLAFIPIFFGTS 809

Qy  482 QSADKLYIQTTLTVSVSLSASVSLGMLYMPKVYIILFHPQNVPKRKSILKAVVTAATM 541
Db  810 QSADKLYIQTTLTVSVSLSASVSLGMLYMPKVYIILFHPQNVPKRKSILKAVVTAATM 869

Qy  542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db  870 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 912

RESULT 6
US-08-855-146-2
; Sequence 2, Application US/08855146
; Patent No. 6221609
; GENERAL INFORMATION:
; APPLICANT: Belagaje, Rama M.
; APPLICANT: Wu, Su
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Department
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,146
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,243
FILING DATE: 07-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-10836
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-6334
TELEFAX: (317) 276-2764
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-855-146-2

Query Match          76.3%; Score 2370; DB 3; Length 908;
Best Local Similarity 75.0%; Pred. No. 5.5e-231;
Matches 437; Conservative 58; Mismatches 86; Indels 2; Gaps 2;

Qy  3 GVSSSLPRTMT-SGFDRYFSSRTLDNNRNWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db  327 GAVTILPKRASIDGDFRYFSSRTLDNNRNWFAEFWEEFGCKLSHG-KENSHIKKCT 385

Qy  62 NRERIGDSAYEQGKQVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLKY 121
Db  386 GLERIASDSSVEQEGKQVQFVIDAVYSNAYALHNNHKDLCPGYIGLCPRMSTIDGKELGY 445

Qy  122 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERQWP 181
Db  446 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYITNKSTYKVIQHTWNLQLHVKVEDMOWA 505

Qy  182 GSGQOLPRISCSLPCQGERKKTVMGMAACWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 241
Db  506 HREHTHPASVCSLPCKEGKKTVMGVPCCWHCEPCEGYNVQVDELSCELCPLDQRPNN 565

Qy  242 RTSQOPIPIVKLEWDSWAVLPLFVAVVGIATLTVVVTFRVYNDTPIVKASGRELSYVL 301
Db  566 RTGCOLIPIIKLEWDSWAVVFPVAILGIATLTVVVTFRVYNDTPIVRASGRELSYVL 625

Qy  302 LAGIFLCYATFLMIABPDLTGCSLRIRIFLGLGMSISYAALLTKTNRIYRIFEQKRSVS 361
Db  626 LTGIFLCYSITFLMIAAPDTIICSFRRVFLGLGCMCFYAALLTKTNRIHRIFEQKKSVT 685

Qy  362 APRISPASOLAITFILISLQLLGCIVFWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 421
Db  686 APKEISPASQLVITFSLISVQLLGCVFWFVVDPPHIIIDYGEQRTLDRPEKARGVLKCDIS 745

Qy  422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPETFEAKPIGFTMYTTCIWLAFIPIFFGTS 481
Db  746 DLSLICSLGYSIILMVTCTVYANKTRGVPETFEAKPIGFTMYTTCIWLAFIPIFFGTA 805

Qy  482 QSADKLYIQTTLTVSVSLSASVSLGMLYMPKVYIILFHPQNVPKRKSILKAVVTAATM 541
Db  806 QSAEKMYIQTTLTVSNMLSASVSLGMLYMPKVYIILFHPQNVQKRRSPKAVVTAATM 865

Qy  542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db  866 QSKLIQKGNDRPNGEAKSELCELENLETPALATKQTYVYTNHAI 908

RESULT 7
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```
US-08-823-110-1
; Sequence 1, Application US/08823110
; Patent No. 607675
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,110
; FILING DATE: March 24, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,298
; FILING DATE: February 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-823-110-1

Query Match 74.9%; Score 2328; DB 3; Length 908;
Best Local Similarity 76.0%; Pred. No. 1e-226;
Matches 430; Conservative 53; Mismatches 81; Indels 2; Gaps 2;

QY 3 GVSSSLPRMT-SGDRVPSSTLNNRRNTWFAEFWEDNFCKLSRLHKKGSHKKCT 61
DB 327 GAVTILPKRASIDGDFRFRSTRNNRRNVWFAEFWEENFGCKLGSHG-KRNSHIKKCT 385
QY 62 NRERIGQDSAYEQEGKVQFVIDAVYAMGHAMHARDLCPGRVGLCPRMDDPDVGTQLKY 121
DB 386 GLERARUSSVEQEGKVQFVIDAVYSMAVALHNMKDLCPGVIGLCPRMSTIDGKELGY 445
QY 122 IRNVNFGSIAGNPVTFNENGDAAPGRYDIYQQLRNGSABYKVGISWTDHLHLRIERMQWP 181
DB 446 IRNVNFGSAGTPVTFNENGDAAPGRYDIYQQLRNGSABYKVGISWTDHLHLRIERMQWP 505
QY 182 GSGQQLPRISICLPQCPQERKKTVMACCHCECTGYQYQVDYCTCTCPYDMRPTE 241
DB 506 HREHTHPASVCLPCKPGERKKTVMACCHCECTGYQYQVDYCTCTCPYDMRPTE 565
QY 242 RTSCQPIPIVKLEWSPNAPVPLFLAVVGIATLFWVTFVRYNDTPIVKASGRELSVYL 301
DB 566 RTGCOLIPIIKLEWSPNAPVPLFLAVVGIATLFWVTFVRYNDTPIVKASGRELSVYL 625

US-08-604-298-1
; Sequence 1, Application US/08604298
; Patent No. 6084084
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,298
; FILING DATE: February 21, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-604-298-1

Query Match 74.9%; Score 2328; DB 3; Length 908;
Best Local Similarity 76.0%; Pred. No. 1e-226;

QY 302 LAGIFLCYATTFMTAEEDLCTCSIRIFPLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
DB 626 LTGIFLCYSITFLMIAAPDTTICSFRRVFLGLGMCFSYAALLTKTNRIHRIPEOGKRSVT 685
QY 362 APRFISPASQLAITFILISLQLLGICVWVFWVDPSPSHSVVDFOQRTLDPRFARGVLKCDIS 421
DB 686 APKFISPASQLVITFSLISVQLLGCVFWVFWVDPSPSHSVVDFOQRTLDPEKARGVLKCDIS 745
QY 422 DLSLICLLGYSNLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAPIPIPGTS 481
DB 746 DLSLICSLGYSILLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAPIPIPGTS 805
QY 482 OSADKLYIQTTLTVSVLSASVSIGMLYMPKVYIILPHBONVPRKRSKAVVTAATM 541
DB 806 QSAEKMYIQTTLTVSVLSASVSIGMLYMPKVYIILPHBONVPRKRSKAVVTAATM 865
QY 542 SNKFTQKGNFRPNGEAKSELCELET 567
DB 866 QSKLIQKGNDRPNGEAKSELCELET 891

RESULT 8
US-08-604-298-1
; Sequence 1, Application US/08604298
; Patent No. 6084084
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,298
; FILING DATE: February 21, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-604-298-1

Query Match 74.9%; Score 2328; DB 3; Length 908;
Best Local Similarity 76.0%; Pred. No. 1e-226;
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Matches	430;	Conservative	53;	Mismatches	81;	Indels	2;	Gaps	2;
Qy	3	GVSSSLPTRMT-SGDFRYSRTLDNRRNIIWFAEFWEDNFHCKLSRHALKGSHIKKCT	61	:	:	:	:	:	:
Db	327	GAVTILPKRASIDGDFRYSRTLDNRRNVWFAEFWEEFGCKLGSHG-KRNSHIKKCT	385	:	:	:	:	:	:
Qy	62	NRRIQDSAYEQBGKQVQFVIDAVYANGHALHAMHRDLCPGRVGLCPRMPDVPDQTLLKY	121	:	:	:	:	:	:
Db	386	GLERIAARDSYEQBGKQVQFVIDAVYSMAYALHNHMKDLCPGYILGCPRMSTIDGKELGY	445	:	:	:	:	:	:
Qy	122	IRNVNFGSIAGNPVTYFNENGADPGRYDIIQYQLRANGSAEYKVIQSWTDHLHLRIERMOWP	181	:	:	:	:	:	:
Db	446	IRAVNFGSAGTPVTYFNENGADPGRYDIFQYQITNKSTEYKVIQHWNTQHLHKVEDQWQA	505	:	:	:	:	:	:
Qy	182	GSQQLPRISICSLPCQGERKKTVKGMACCMHCEPCTGYQYQVDRYTCKTCPYDMRPTEN	241	:	:	:	:	:	:
Db	506	HREHTHPASVCSLPCPKGERKKTVKGVPCWCHCERCERYNQVDELSCELCPLDORPMN	565	:	:	:	:	:	:
Qy	242	RTSCQPTPIVKLEWDSWPAVLPLFLAVVGTAAATLFWVVTFRYNDTPIVKASGRELSSVL	301	:	:	:	:	:	:
Db	566	RTGQLPIPIKLEWHSPWAVPVFAVILGTIATTFVITFVRYNDTPIVRASGRELSSVL	625	:	:	:	:	:	:
Qy	302	LAGIFLCVATTFMLIABPDLTGCSLRIFILGLGMSISVAALLTKNRIYRIFEOGKRSVS	361	:	:	:	:	:	:
Db	626	LTGIFLCYSITFLMIAPDTIICSFRVFFLGLGNCFSYAALLTKNRIHRIFEOGKKSVT	685	:	:	:	:	:	:
Qy	362	APRFPASQLAITFIIISLQLLGICVWVVDPSHVSVDFOQRTLDPRFARGVLKCDIS	421	:	:	:	:	:	:
Db	686	APKFPISASQLVITFSLISVQLLGIVFWVVDPPHIIIDYGEQRTLDPEKARGVLKCDIS	745	:	:	:	:	:	:
Qy	422	DLSLIICLLGYSMLLMWCTVYAIKTRGVPEFNEAKPIGFTMYTTCIWLAFPIFGTS	481	:	:	:	:	:	:
Db	746	DLSLIICSLGYSILLMWCTVYAIKTRGVPEFNEAKPIGFTMYTTCIWLAFPIFGTA	805	:	:	:	:	:	:
Qy	482	QSAKLYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFHPBQNVPKRSLKAVVTAATM	541	:	:	:	:	:	:
Db	806	QSAEKWYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFHPBQNVQKRKSFKAVVTAATM	865	:	:	:	:	:	:
Qy	542	SNKPTQKGNFRPNGEAKSELCEINLET	567	:	:	:	:	:	:
Db	866	QSKLIOKGNDRPNGEAKSELCESET	891	:	:	:	:	:	:

RESULT 9
US-08-617-785-12
; Sequence 12, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-12

	Best Local Similarity	69.9%	Pred.	No.	1.2e-215;		
	Matches	408;	Conservative	74;	Mismatches	100;	
					Indels	2; Gaps	2;
Qy	3 GVSSSPTRMT-SGFDRYSSRRLDNNRNINFAEFWEONFHCKLSRHALKGSHLKCT	61					
Dd	332 GAITIQQKRAIVGGDFAYFSRTLENNRRNVNVAEYWEENFNCKLTISGSKKEDTDKCT	391					
Qy	62 NNRERGDSAYBEGKVQFVIDAVYANGHALHAMHRDLCPGRVGLCPRMDPDVDGTOLLKY	121					
Dd	392 QGERIGKSDNYEBGVQFVIDAVYAMAHALHMNDLDCADYRGVCPEMEQAAGKLLKY	451					
Qy	122 IRNVFGSIAGNPVTWNEGDARGDYDIYOYLNGS-AEKVIQSWTDLHLRIERMOW	180					
Dd	452 IRNVNFSGAGTVMFNKGDAFGRDYIIFQYTNTSNPGYRILGIQMTELQNIEDMOW	511					
Qy	181 PGSQOUPRICSLPCOPSERKKTAKGMACWHCEPCTGYQOVDRYTKTCIPYDMRPTE	240					
Dd	512 KGKVEIPAASCVCLPKCKQGOKTKTGTPCCWCETCDGVOGFDEMTQHCHPYDORPNE	571					
Qy	241 NRTSQCPIPVKLWDSPMAVLPLFLAVGIIAATLFVVVFTRYNDPTPIVKASGRELSYV	300					
Dd	572 NR TGCGDIPITIKLEHSPNAVIPVFLAMLGITAFIMMATFIYNPTPIVRASGRELSYV	631					
Qy	301 LLACIFLCVATTMLTAEPDLGCSSLRRIFLGISMISYAALLTKTNIRYRIFEQSKRSV	360					
Dd	632 LLYGIFYCYTIITELMIAPDVAVCSPPRFVLGUMGISYAALLUTKNRIYRIFEQSKSV	691					
Qy	361 SAPFRISPASQLAITFILISLQLLGICWFVDPDPSHVDFQDQRTLDPREFARGVLKCDI	420					
Dd	692 TAPRLISPTSOLAITSSLISSVQLLVGFVFWGVDDPNIIIDYDEHKTMNQEQARGVLKCDI	751					
Qy	421 SDLSLICLLGYSMLMVTVTYAIATRGPVPETEAEKPFGFTMYTTTCIWLAPIPFPGT	480					
Dd	752 TDLOIICS LGSYILLMVTVTYAIATRGPVENFEAREKFPTMYTTTCIWLAPIPFPGT	811					
Qy	481 SQSADKIYIOTTTTVSYSLASVSLGMLMPKVYIILFHPGEONVPRKRSLKAUVTAAT	540					
Dd	812 AQSAEKDIYOTTTITSMNLUSAVGLMLPMKVYIIIHFPELNUNQKRKSRFKAVUAAAT	871					
Qy	541 MSNKFTQGNFRPNGEAKSELLENLETPALATKQTYYTVTTHAI	584					
Dd	872 MSSRLSHKPSDRNGEAKELTCELCEVNPDNSPAACKKVVSYNNLVI	915					
 RESULT 10 US-09-817-464-12 Sequence 12, Application US/09817464 Patent No. 6515107 GENERAL INFORMATION: Applicant: Flor, Peter J. ApplcAnt: Kuhn, Ranier ApplcAnt: Lindaur, Kristen ApplcAnt: Puttner, Irene ApplcAnt: Knopfcl, Thomas TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4, TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds FILE REFERENCE: 4-19679/A/PCT CURRENT APPLICATION NUMBER: US/09/817,464 CURRENT FILING DATE: 2001-03-26 EARLIER APPLICATION NUMBER: US/08/617,785 EARLIER FILING DATE: 1996-03-19 EARLIER APPLICATION NUMBER: EPO 9416553.7 EARLIER FILING DATE: 1994-08-19 EARLIER APPLICATION NUMBER: EPO 93810663.0 EARLIER FILING DATE: 1993-09-20 NUMBER OF SEQ ID NOS: 26 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 12 LENGTH: 915 TYPE: PRT ORGANISM: Homo sapiens US-09-817-464-12							

Query Match 71.4%; Score 2219; DB 4; Length 915;
Best Local Similarity 69.9%; Pred. No. 1.2e-215;
Matches 408; Conservative 74; Mismatches 100; Indels 2; Gaps 2;

QY 3 GVSSSLPTMT-SGPDYFSSRTLNNRRNIWFAEFWEDNFHCKLSRHAKKGSHKCT 61
DB 332 GAITIQPKATVEGDAYFTSRTLENNRRNVFAEYWEENFNCKLTISGSKEDTRDKT 391

QY 62 NRERIGQDSAYEQEGKQVQFVIDAVYAMGHALHAMRDLCPCRGVGLCPRMDPVDGTQLLKY 121
DB 392 QGERIGKDSNYEQEGKQVQFVIDAVYAMAHALHNNKDLCADYRGVCPMEQAGGKLLKY 451

QY 122 IRNVNFGSIAGNVTFFNENGDA PGYDIYQYQLRNGS-AEYKIVGSWTDHLRLRERMOW 180
DB 452 IRNVNFGSAGTVPVFNKNGDAPGRYDIYQYQTTNTNSPGYRLIGQWTDLQNLNEDMOW 511

QY 181 PGSGQOLPRISCLPCOPGERKTKVGMACWHCEPCTGYQYQVDRYCTKCTPYDMRPT 240
DB 512 KGKVEIPASVCTLPCPKGQRKTKQKTPCCWTCPCDGYQYQFDEMTCHQCPYQORPNE 571

QY 241 NRTSQPIPIVKLEWDSMAVLPFLAVVGGIAATLFFVVVTFVRYNDTPIVKAAGRELSYV 300
DB 572 NRTGQDPIIKLEWHSMAVLPFLAVVGGIAATLFFVMAATFIRYNDTPIVKAAGRELSYV 631

QY 301 LLAGIFLCYATTFMLAEPDLGTSRLRIFLGLGMSISYAALLTKTNRIYRIFEGQKRSV 360
DB 632 LLTGIFLCYIITFLMAKPDVAVCSFRVFLGLGMCISYAALLTKTNRIYRIFEGQKRSV 691

QY 361 SAPRISPASOLAITFILISLQLLGICVWFVVDPSHSVVDFOQRTLDPRFARGVLKCDI 420
DB 692 TAPRLISPTSQLAITSLSISVQLLGIVFWGVDPPNIIIDYDEHKTMPQEQARGVLKCDI 751

QY 421 SDLSLICLLGYSLMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPIFFT 480
DB 752 TDLQIICSLGYSLMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPIFFT 811

QY 481 SOSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQNVKPKRSUKAVVTAAT 540
DB 812 AQSAEKLYIQTTLTISMLNSASVALGMLYMPKVYIILFHPELNVQKRSKPAVVTAAT 871

QY 541 MSNKFTQGNFRPNPGEAKSELCELETALATKQYVTVYTNHAI 584
DB 872 MSSRLSHKPSDRPNPGEAKTELCELVDPNSPAKKKYVSNNLVI 915

RESULT 11

US-08-453-862-2
; Sequence 2, Application US/08453862
; Patent No. 5738999
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,862
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 436

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-862-2

Query Match 71.1%; Score 2210; DB 1; Length 915;
Best Local Similarity 69.5%; Pred. No. 9.5e-215;
Matches 406; Conservative 76; Mismatches 100; Indels 2; Gaps 2;

QY 3 GVSSSLPTMT-SGPDYFSSRTLNNRRNIWFAEFWEDNFHCKLSRHAKKGSHKCT 61
DB 332 GAITIQPKATVEGDAYFTSRTLENNRRNVFAEYWEENFNCKLTISGSKEDTRDKT 391

QY 62 NRERIGQDSAYEQEGKQVQFVIDAVYAMGHALHAMRDLCPCRGVGLCPRMDPVDGTQLLKY 121
DB 392 QGERIGKDSNYEQEGKQVQFVIDAVYAMAHALHNNKDLCADYRGVCPMEQAGGKLLKY 451

QY 122 IRNVNFGSIAGNVTFFNENGDA PGYDIYQYQLRNGS-GSAEYKIVGSWTDHLRLRERMOW 180
DB 452 IRNVNFGSAGTVPVFNKNGDAPGRYDIYQYQTTNTNPGYRLIGQWTDLQNLNEDMOW 511

QY 181 PGSGQOLPRISCLPCOPGERKTKVGMACWHCEPCTGYQYQVDRYCTKCTPYDMRPT 240
DB 512 KGKVEIPSSVCTLPCPKGQRKTKQKTPCCWTCPCDGYQYQFDEMTCHQCPYQORPNE 571

QY 241 NRTSQPIPIVKLEWDSMAVLPFLAVVGGIAATLFFVVVTFVRYNDTPIVKAAGRELSYV 300
DB 572 NRTGQDPIIKLEWHSMAVLPFLAVVGGIAATLFFVMAATFIRYNDTPIVKAAGRELSYV 631

QY 301 LLAGIFLCYATTFMLAEPDLGTSRLRIFLGLGMSISYAALLTKTNRIYRIFEGQKRSV 360
DB 632 LLTGIFLCYIITFLMAKPDVAVCSFRVFLGLGMCISYAALLTKTNRIYRIFEGQKRSV 691

QY 361 SAPRISPASOLAITFILISLQLLGICVWFVVDPSHSVVDFOQRTLDPRFARGVLKCDI 420
DB 692 TAPRLISPTSQLAITSLSISVQLLGIVFWGVDPPNIIIDYDEHKTMPQEQARGVLKCDI 751

QY 421 SDLSLICLLGYSLMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPIFFT 480
DB 752 TDLQIICSLGYSLMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPIFFT 811

QY 481 SOSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQNVKPKRSUKAVVTAAT 540
DB 812 AQSAEKLYIQTTLTISMLNSASVALGMLYMPKVYIILFHPELNVQKRSKPAVVTAAT 871

QY 541 MSNKFTQGNFRPNPGEAKSELCELETALATKQYVTVYTNHAI 584
DB 872 MSSRLSHKPSDRPNPGEAKTELCELVDPNSPAKKKYVSNNLVI 915

RESULT 12
US-08-452-734A-2
; Sequence 2, Application US/08452734A
; Patent No. 5831047
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.

Db 572 NRTGCONPIIKLEHSPHAWIPVFLMGLIATIFVWATFIRYNDTPIVRASGRELSTV 631
Qy 301 LLAGIFLCYATTFLMIAEPDLGTSRLRIFLGLGMSISYAAALLTKTNRIRYRIFEOGKRSV 360
Db 632 LLTGIFLCYIITFLMIAKPDVAVCSFRVFLGLGMCISYAAALLTKTNRIRYRIFEOGKRSV 691
Qy 361 SAPRISPASQALATFILISQLLIGICVWFVVDPSHVSVDFOQDRTLPFRFARGVLKCDI 420
Db 692 TAPRLISPTSQALATSSLSISVQLLGVFIWFGVDPENIIIDYDEHKTMRPEQARGVLKCDI 751
Qy 421 SDLSILICLLGYSMLLMVTCVYAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPIFGT 480
Db 752 TDQLIICSLGYSILLMVTCVYAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPIFGT 811
Qy 481 SOSADKLYIQTTLTIVSVLSASVSLGMLYMPKVYIILFHPHQNVPKRKSILKAVVTAAT 540
Db 812 AQSACKLYIQTTLTISNLSASVALGMLYMPKVYIILFHPELNVQKRKSPKAVVTAAT 871
Qy 541 MSNKETQGNFRPNCEAKSELCEULETALATKQTYVYTNHAI 584
Db 872 MSSRLSHKPSDRPNCEAKTELCENVDPNSPAACKKYVSNNLVI 915

RESULT 14

PCT-US94-14989-2
; Sequence 2, Application PC/TUS9414989
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14989-2

Query Match 71.1%; Score 2210; DB 5; Length 915;

Best Local Similarity 69.5%; Pred. No. 9.5e-215;
Matches 406; Conservative 76; Mismatches 100; Indels 2; Gaps 2;

Qy 3 GVSSSLPRMT-SGDRYFSSRTLNNRRNTWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 332 GAITIQKRAIVEGFDAYFTSRTLENNRRNVFAEYWEENFNCKLTISGSKKEDTRDKT 391
Qy 62 NRERIGQDSAYEQGKQVFDIVAYAMGHALHAMHRDLCPRGVGLCPMDPVDGTQLLY 121
Db 392 QGERIGKDSNVEQKQVFDIVAYAMGHALHMNKDLCADYRGVCPMEQAGGKLLKY 451
Qy 122 IRNVNFGIAGNPVTNENGDPGRYDIYQQLRNGS-AEYKVIGSWTDHLHLRIERMOW 180
Db 452 IRNVNFGSAGTPVNFNKGDPGRYDIYQQLRNGS-AEYKVIGSWTDHLHLRIERMOW 511

Qy 191 PGSGOOLPRSTCSLPQGPGRKTKVGMACCHCEPCTGYQVDRYTKCTCPYDMRPT 240
Db 512 GKGVREIPSSVCTLPKPGQRKTKQKTPCCWTCBPCDGYQFQDEMTCQHCPYDQRPNE 571
Qy 241 NRTSCQPIPIKLEWDSMAVLPFLAVVGLAATLPVVVTFVRYNDTPIVKASGRELSTV 300
Db 572 NRTGCONPIIKLEHSPHAWIPVFLMGLIATIFVWATFIRYNDTPIVRASGRELSTV 631
Qy 301 LLAGIFLCYATTFLMIAEPDLGTSRLRIFLGLGMSISYAAALLTKTNRIRYRIFEOGKRSV 360
Db 632 LLTGIFLCYIITFLMIAKPDVAVCSFRVFLGLGMCISYAAALLTKTNRIRYRIFEOGKRSV 691
Qy 361 SAPRISPASQALATFILISQLLIGICVWFVVDPSHVSVDFOQDRTLPFRFARGVLKCDI 420
Db 692 TAPRLISPTSQALATSSLSISVQLLGVFIWFGVDPENIIIDYDEHKTMRPEQARGVLKCDI 751
Qy 421 SDLSILICLLGYSMLLMVTCVYAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPIFGT 480
Db 752 TDQLIICSLGYSILLMVTCVYAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPIFGT 811
Qy 481 SOSADKLYIQTTLTIVSVLSASVSLGMLYMPKVYIILFHPHQNVPKRKSILKAVVTAAT 540
Db 812 AQSACKLYIQTTLTISNLSASVALGMLYMPKVYIILFHPELNVQKRKSPKAVVTAAT 871
Qy 541 MSNKETQGNFRPNCEAKSELCEULETALATKQTYVYTNHAI 584
Db 872 MSSRLSHKPSDRPNCEAKTELCENVDPNSPAACKKYVSNNLVI 915

RESULT 15

US-08-617-785-4
; Sequence 4, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Fluor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-4

Query Match 70.5%; Score 2191.5; DB 3; Length 867;

Best Local Similarity 69.3%; Pred. No. 6.6e-213;
Matches 405; Conservative 73; Mismatches 99; Indels 7; Gaps 3;

Qy 3 GVSSSLPRMT-SGDRYFSSRTLNNRRNTWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 277 GAITIQKRAIVEGFDAYFTSRTLENNRRNVFAEYWEENFNCKLTISGSKKEDTRDKT 336
Qy 62 NRERIGQDSAYEQGKQVFDIVAYAMGHALHAMHRDLCPRGVGLCPMDPVDGTQLLY 121
Db 337 QGERIGKDSNVEQKQVFDIVAYAMGHALHMNKDLCADYRGVCPMEQAGGKLLKY 396
Qy 122 IRNVNFGIAGNPVTNENGDPGRYDIYQQLRNGS-AEYKVIGSWTDHLHLRIERMOW 180
Db 397 IRNVNFGSAGTPVNFNKGDPGRYDIYQQLRNGS-AEYKVIGSWTDHLHLRIERMOW 456

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OM protein - protein search, using sw model

Run on: June 17, 2005, 17:59:08 ; Search time 165 Seconds
(without alignments)
1368.897 Million cell updates/sec

Title: US-10-828-332-7

Perfect score: 3107

Sequence: 1 MPGVSSLPRTMTSGFDYF.....LETPALATKQYVYVTHAI 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3107	100.0	584	6	ABR56244 Rat gluta
2	3050.5	98.2	604	6	ABG74133 Rat metab
3	3050.5	98.2	912	7	ADG58164 Rat Prote
4	3050.5	98.2	912	7	ADG58168 Rat Prote
5	3017	97.1	909	8	ADO29095 Mouse nov
6	3004.5	96.7	909	5	AAOI5101 Human pns
7	3004.5	96.7	912	2	AAR82658 Human mgl
8	3004.5	96.7	912	5	AAR23757 Human met
9	3004.5	96.7	912	6	ABP81846 Human met
10	3004.5	96.7	912	7	ADG58170 Human pro
11	3004.5	96.7	912	7	ADG58166 Human pro
12	3004.5	96.7	912	8	ADO29094 Human nov
13	3004.5	96.7	912	8	ADG89114 Human uro
14	3001.5	96.6	912	2	AAR72092 Human mgl
15	2912.5	93.7	591	8	ADR08623 Human pro
16	2852.5	91.8	886	8	ABM84666 Human dia
17	2719	87.5	796	8	ADR10452 Human pro
18	2713	87.3	862	8	ABM84667 Human dia
19	2710.5	87.2	1422	5	AAOI5102 Human phm
20	2377	76.5	908	6	ABR62488 Human met
21	2377	76.5	908	8	ABR62489 Human met
22	2377	76.5	908	8	ADO29476 Human gpc
23	2374	76.4	908	6	ABR62490 Human met
24	2370	76.3	908	2	AAW41568 Human met
25	2370	76.3	908	5	ABB09564 Human GRM

26	2370	76.3	908	6	ABP81850 Human met
27	2370	76.3	908	7	ADE31729 Human 235
28	2370	76.3	908	8	ADG89128 Human uro
29	2369	76.2	908	6	ABR62491 Human met
30	2348	75.6	1142	4	ABG29451 Novel hum
31	2336	75.2	908	8	ADO29477 Mouse gpc
32	2328	74.9	908	2	AAW49928 Human met
33	2328	74.9	913	4	ABG29452 Novel hum
34	2219	71.4	915	5	ABG95155 Human gpc
35	2219	71.4	915	6	ABP81849 Human met
36	2219	71.4	915	7	ADG55969 Human pro
37	2219	71.4	915	7	ADJ93191 Human met
38	2219	71.4	915	8	ADO29103 Human nov
39	2215	71.3	915	2	AAR72097 Human mgl
40	2214	71.3	915	5	ABG95164 Human gpc
41	2214	71.3	915	8	ADO29104 Mouse nov
42	2213	71.2	915	5	ABG95165 Human gpc
43	2212	71.2	915	5	ABG95166 Human gpc
44	2210	71.1	915	2	AAR80479 Rat metab
45	2210	71.1	915	6	AAE30199 Rat metab

ALIGNMENTS

RESULT 1

ABR56244
ID ABR56244 standard; protein; 584 AA.

XX ABR56244;

AC ABR56244;

XX 20-NOV-2003 (first entry)

DT Rat glutamic acid receptor.

DE Rat glutamic acid receptor.

XX Rat glutamic acid receptor.

KW Rat; anorectic; antiulcer; antidiabetic; laxative; antidiarrheic;

KW Glutamic acid receptor; receptor; gastrointestinal tract disorder;

KW sitleirgia; obesity; ulcer; diabetes; constipation; diarrhoea.

XX Rattus norvegicus.

XX WO2003035873-A1.

XX 01-MAY-2003.

XX 23-OCT-2002; 2002WO-JP010984.

XX 23-OCT-2001; 2001JP-00325159.

XX (AJIN) AJINOMOTO CO INC.

XX San Gabriel A, Maekawa T, Uneyama H, Torii K;

XX WPI; 2003-430418/40.

XX N-PSDB; ACC70676.

XX Novel glutamic acid receptor protein and encoded DNA, applicable in

XX screening agonists or antagonists of glutamic acid or allosteric

XX modulator for use as drugs in ameliorating symptoms and diseases e.g.

XX obesity.

XX Claim 3; Page 33-35; 39pp; Japanese.

XX The present sequence is the protein sequence for rat glutamic acid

XX receptor. The receptor has a transmembrane domain and an intracellular

XX domain common to type 4 metabotropic glutamic acid receptor protein, and

XX an extracellular domain shorter by 316 or 327 amino acid residues than

XX type 4 metabotropic glutamic acid receptor protein. The receptor and its

XX coding sequence are useful in screening agonists or antagonists of

XX glutamic acid or allosteric modulator for use as drugs in ameliorating

XX symptoms and diseases due to abnormal metabolism in gastrointestinal

XX tract including small and large intestines e.g. sitleirgia, obesity,

XX ulcer, diabetes, constipation and diarrhoea


```

XX SQ Sequence 584 AA;
Query Match 100.0%; Score 3107; DB 6; Length 584;
Best Local Similarity 100.0%; Pred. No. 6.4e-314;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPGVSSSLPTMTSGFDRYFSSRTLDNNRNIWFAEFWEDNFHCKLSRHALKKGSHIKKC 60
Db 1 MPGVSSSLPTMTSGFDRYFSSRTLDNNRNIWFAEFWEDNFHCKLSRHALKKGSHIKKC 60

Qy 61 TNRRIGQDSAYEQEGKQVQFVIDAVYANGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLK 120
Db 61 TNRRIGQDSAYEQEGKQVQFVIDAVYANGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLK 120

Qy 121 YIRNVNFSGIAGNPVTFNENGDAFGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERQW 180
Db 121 YIRNVNFSGIAGNPVTFNENGDAFGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERQW 180

Qy 181 PGSGQQLPRISCSLPCQGERKKTVMGACWCHCEPCTGYQYQVDRYTKCTCPYDMRPT 240
Db 181 PGSGQQLPRISCSLPCQGERKKTVMGACWCHCEPCTGYQYQVDRYTKCTCPYDMRPT 240

Qy 241 NRTSQPIPIVKLEWDSWAVLPLFLAVVGGIAATLFFVVVTFVRYNDTPIVKASGRELSYV 300
Db 241 NRTSQPIPIVKLEWDSWAVLPLFLAVVGGIAATLFFVVVTFVRYNDTPIVKASGRELSYV 300

Qy 301 LLAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKNRIYRIFEQGRSV 360
Db 301 LLAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKNRIYRIFEQGRSV 360

Qy 361 SAPREISASQALATFILLISQLLIGICVWFVVDPSHVSVDQDQRTLDPRFARGVLKCDI 420
Db 361 SAPREISASQALATFILLISQLLIGICVWFVVDPSHVSVDQDQRTLDPRFARGVLKCDI 420

Qy 421 SDLSLICLLGYSMILMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPFPGT 480
Db 421 SDLSLICLLGYSMILMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPFPGT 480

Qy 481 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAAT 540
Db 481 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAAT 540

Qy 541 MSNFKTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db 541 MSNFKTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584

RESULT 2
ABG74133
ID ABG74133 standard; protein; 604 AA.
XX
AC ABG74133;
XX
DT 03-APR-2003 (first entry)
XX
DE Rat metabotropic glutamate receptor mGluR4.
XX
KW Rat; metabotropic glutamate receptor; mGluR4; umami; taste; receptor;
KW umami mimicking compound; monosodium L-glutamate; CAMP.
XX
OS Rattus sp.
XX
FN US2002151052-A1.
XX
PD 17-OCT-2002.
XX
PF 30-MAR-2001; 2001US-00820809.
XX
PR 31-MAR-2000; 2000US-0193454P.
XX
PA (UYMI-) UNIV MIAMI.
XX

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PI Chaudhari N, Roper SD;
XX WPI: 2003-182515/18.
XX N-PSDB; ABX16077.
XX Novel metabotropic glutamate taste receptor which functions as a umami
XX taste receptor, useful for screening for umami mimicking compounds.
XX Claim 1; Page 7; 23pp; English.
XX The invention relates to a rat metabotropic glutamate taste receptor
XX having a molecular weight of 68 kDa, mGluR4, appearing as ABG74133. Also
XX included are an isolated mRNA molecule encoding mGluR4 appearing as
XX ABX16077 (rat sequence) and the human homologue appearing as ABX16087, a
XX mammalian cell transfected with cDNA encoding mGluR4 (the cDNA expressed
XX in the mammalian cell is capable of being translated into immunologically
XX recognisable metabotropic glutamate taste receptors) and screening
XX samples for umami mimicking compounds (comprising: (a) transfecting
XX mammalian cells with an isolated rat cDNA encoding metabotropic glutamate
XX taste receptor; (b) culturing the transfected cells in an environment
XX that promotes expression of immunologically recognisable metabotropic
XX glutamate taste receptors; (c) treating the transfected cells with a
XX compound that induces CAMP production; (d) incubating the cells with a
XX sample containing a potential umami mimicking compound capable of binding
XX to the metabotropic glutamate taste receptors; (e) measuring the amount
XX of CAMP produced; and (f) correlating suppression of CAMP production with
XX umami mimicking compound binding to the metabotropic glutamate taste
XX receptors). The mGluR4 functions as a umami taste receptor, and responds
XX to monosodium L-glutamate binding by decreasing cellular level of CAMP.
XX The cell is useful for screening samples for umami mimicking compounds.
XX The mGluR4 is useful for screening for umami mimics. The present sequence
XX represents the rat mGluR4 protein
XX Sequence 604 AA;
SQ

```

```

Query Match 98.2%; Score 3050.5; DB 6; Length 604;
Best Local Similarity 98.6%; Pred. No. 5.2e-308;
Matches 575; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 3 GVSSSLPTMT-SGFDRYFSSRTLDNNRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 22 GAVTILPKRMSVGRGDFYFSSRTLDNNRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 81

Qy 62 NRERIGQDSAYEQEGKQVQFVIDAVYANGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLK 121
Db 82 NRERIGQDSAYEQEGKQVQFVIDAVYANGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLK 141

Qy 122 IRNVNFSGIAGNPVTFNENGDAFGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERQW 181
Db 142 IRNVNFSGIAGNPVTFNENGDAFGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERQW 201

Qy 182 GSGQQLPRISCSLPCQGERKKTVMGACWCHCEPCTGYQYQVDRYTKCTCPYDMRPTEN 241
Db 202 GSGQQLPRISCSLPCQGERKKTVMGACWCHCEPCTGYQYQVDRYTKCTCPYDMRPTEN 261

Qy 242 RTSCQPIPIVKLEWDSWAVLPLFLAVVGGIAATLFFVVVTFVRYNDTPIVKASGRELSYV 301
Db 262 RTSCQPIPIVKLEWDSWAVLPLFLAVVGGIAATLFFVVVTFVRYNDTPIVKASGRELSYV 321

Qy 302 LAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKNRIYRIFEQGRSVS 361
Db 322 LAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKNRIYRIFEQGRSVS 381

Qy 362 APRFISASQALATFILLISQLLIGICVWFVVDPSHVSVDQDQRTLDPRFARGVLKCDIS 421
Db 382 APRFISASQALATFILLISQLLIGICVWFVVDPSHVSVDQDQRTLDPRFARGVLKCDIS 441

Qy 422 DLSLICLLGYSMILMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPFPGTS 481
Db 442 DLSLICLLGYSMILMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPFPGTS 501

Qy 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAAT 541

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Db 502 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPEQNVPKRSLKAVVTAATM 561
 QY 542 SNKFTQKGNFRPNGBEAKSELNLETPALATKQTVYTYTNHAI 584
 Db 562 SNKFTQKGNFRPNGBEAKSELNLETPALATKQTVYTYTNHAI 604

RESULT 3
 ADE58164
 ID ADE58164 standard; protein; 912 AA.
 AC ADE58164;
 XX
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein P31423, SEQ ID NO 4035.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'ureo D, Befort K, Costigan M;
 XX
 XX WPI; 2003-268312/26.
 DR GENBANK; P31423.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 912 AA;
 Query Match 98.2%; Score 3050.5; DB 7; Length 912;
 Best Local Similarity 98.6%; Pred. No. 9.7e-308;
 Matches 575; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 QY 3 GVSSSLPTMT-SGPDYFSSRTLDNRRNTWFAEFWEDNFHCKLSRHAKKGSHIKKCT 61
 Db 330 GAVTILPKRMSVRGPDYFSSRTLDNRRNTWFAEFWEDNFHCKLSRHAKKGSHIKKCT 389
 QY 62 NRERIGQDSAYEQEGKQVFDVAVYAMGHALHAMERDLCPCRGVGLCPRMDPVDGTQLLKY 121
 Db 390 NRERIGQDSAYEQEGKQVFDVAVYAMGHALHAMERDLCPCRGVGLCPRMDPVDGTQLLKY 449
 QY 122 IRNVNFSIAGNPVTFNENGDAPEGRIYQVQLRNGSAEYKVGISWTDLHLRIERMOWP 181
 Db 450 IRNVNFSIAGNPVTFNENGDAPEGRIYQVQLRNGSAEYKVGISWTDLHLRIERMOWP 509
 QY 182 GSGQQLPRSIICSLPCQGERKKTVMGMACCHCEPCTGYOVQVDRYTKCTCPYDMRPTEN 241
 Db 510 GSGQQLPRSIICSLPCQGERKKTVMGMACCHCEPCTGYOVQVDRYTKCTCPYDMRPTEN 569
 QY 242 RTSCQPIPIVKLEWDSWAVLPLFLAVVGIATLFWVVTFRYNDTPIVKASGRELSYVL 301
 Db 570 RTSCQPIPIVKLEWDSWAVLPLFLAVVGIATLFWVVTFRYNDTPIVKASGRELSYVL 629
 QY 302 LAGIFLCYATTFLMTAEPDLGTCSLRRIFPLGLGMSISYAALLTKTNRIYRIPEQGRSVS 361
 Db 630 LAGIFLCYATTFLMTAEPDLGTCSLRRIFPLGLGMSISYAALLTKTNRIYRIPEQGRSVS 689
 QY 362 APRFISPASOLAITEFILISLQLLGCVMFVVDPSHSVDFODORTLDRPARGVLKCDIS 421
 Db 690 APRFISPASOLAITEFILISLQLLGCVMFVVDPSHSVDFODORTLDRPARGVLKCDIS 749
 QY 422 DLSLILCLGYSMLLMVTCTVYAIKTRGVPETNEAKPIGFTMYTTCIVMLAFIPIPFPGTS 481
 Db 750 DLSLILCLGYSMLLMVTCTVYAIKTRGVPETNEAKPIGFTMYTTCIVMLAFIPIPFPGTS 809
 QY 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPEQNVPKRSLKAVVTAATM 541
 Db 810 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPEQNVPKRSLKAVVTAATM 869
 QY 542 SNKFTQKGNFRPNGBEAKSELNLETPALATKQTVYTYTNHAI 584
 Db 870 SNKFTQKGNFRPNGBEAKSELNLETPALATKQTVYTYTNHAI 912

RESULT 4
 ADE58168
 ID ADE58168 standard; protein; 912 AA.
 XX
 AC ADE58168;
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein P31423, SEQ ID NO 4039.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEO) GEN HOSPITAL CORP.

CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 909 AA;

Query Match 97.1%; Score 3017; DB 8; Length 909;
 Best Local Similarity 97.8%; Pred. No. 3e-304;
 Matches 570; Conservative 3; Mismatches 8; Indels 2; Gaps 2;

QY 3 GVSSSLPTMT-SGDRYFSSRTLDNNRNINFAEFWEDNFHCKLSRHALKGSHIKKCT 61
 DB 328 GAVTILPKRTSRGDRYFSSRTLDNNRNINFAEFWEDNFHCKLSRHALKGSHIKKCT 387

QY 62 NREICGDSAYEKGKQVFDVAVYAMGHALHAMHDLCPGRVGLCPMDPDVGTOLLY 121
 DB 388 NREICGDSAYEKGKQVFDVAVYAMGHALHAMHDLCPGRVGLCPMDPDVGTOLLY 447

QY 122 IRNVNFSGIAGNPVTNENGAPGRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERMOWP 181
 DB 448 IRNVNFSGIAGNPVTNENGAPGRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERMOWP 507

QY 182 GSGQQLPRISLPCQPGERKKTVMGACCHCEPCTGYQYQVDRYTKTCYDMPRTEN 241
 DB 508 GSG-QLPRLSICSLPCQPGERKKTVMGACCHCEPCTGYQYQVDRYTKTCYDMPRTEN 566

QY 242 RTSCQPIPIVKLEWDSWAVLPLFLAVVGIAATLFVVVTFVRYNDTPIVKASGRLSYVL 301
 DB 567 RTSCQPIPIVKLEWDSWAVLPLFLAVVGIAATLFVVVTFVRYNDTPIVKASGRLSYVL 626

QY 302 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 361
 DB 627 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 586

QY 362 APRFISPASQLAITFLISLQLGICVWFVDPSSHVDVDFQDRTLDRPARGVLKCDIS 421
 DB 687 APRFISPASQLAITFLISLQLGICVWFVDPSSHVDVDFQDRTLDRPARGVLKCDIS 746

QY 422 DLSLICLLGYSMLLMTCTVYAIKTRGVPEFNEAKPIGFTWYTTTCIVMLAIPFPGTS 481
 DB 747 DLSLICLLGYSMLLMTCTVYAIKTRGVPEFNEAKPIGFTWYTTTCIVMLAIPFPGTS 806

QY 482 QSADKLYIQTTLTIVSVLSASVSLGMLYMPKYIILFHPQONVPRKESLKAIVTAAATM 541
 DB 807 QSADKLYIQTTLTIVSVLSASVSLGMLYMPKYIILFHPQONVPRKESLKAIVTAAATM 866

QY 542 SNKFTQKGNFRPNGEAKSELNLETPALATKQTYVYTNHAI 584
 DB 867 SNKFTQKGNFRPNGEAKSELNLETPALATKQTYVYTNHAI 909

RESULT 6

AAO15101
 ID AAO15101 standard; protein; 909 AA.
 AC AAO15101;
 XX
 DT 29-AUG-2003 (revised)
 DT 22-AUG-2002 (first entry)
 XX
 XX Human ph8SPmGluR4 chimeric protein.
 DE Human; G-protein fusion receptor; extracellular domain;
 XX transmembrane domain; intracellular domain; Car; mGluR; GABABR;
 KW modulator identification.
 XX
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN WO200229033-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US031074.
 XX
 PR 03-OCT-2000; 2000US-00679664.
 XX
 XX (NPSF-) NPS PHARM INC.
 XX
 XX Storrman T, Hammerland LG, Storjohann LL, Busby JG, Garrett JB;
 PI Simin RT;
 XX
 DR WPI; 2002-330170/36.
 XX
 PT Novel G-protein fusion receptor, useful for identifying modulators of
 PT Car, mGluR and GABABR, comprises G-protein joined to the intracellular
 PT domain of the receptor.
 XX
 PS Disclosure; Fig 16; 168pp; English.
 XX
 CC The invention comprises G-protein fusion receptors - comprising
 CC extracellular, transmembrane and intracellular domains similar to Car,
 CC mGluR or GABAB receptor sequences. The G-protein fusion receptors of the
 CC invention may also possess a linker joined to the carboxy terminus of the
 CC intracellular domain, and a G-protein joined to the linker. The G-protein
 CC fusion receptors of the invention are useful for identifying modulators
 CC of Car, mGluR and GABABR for use in treating associated conditions. The
 CC present amino acid sequence was used in the production of the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 XX Sequence 909 AA;

Query Match 96.7%; Score 3004.5; DB 5; Length 909;
 Best Local Similarity 96.7%; Pred. No. 6e-303;
 Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 3 GVSSSLPTMT-SGDRYFSSRTLDNNRNINFAEFWEDNFHCKLSRHALKGSHIKKCT 61
 DB 327 GAVTILPKRMSVRGDRYFSSRTLDNNRNINFAEFWEDNFHCKLSRHALKGSHIKKCT 386

QY 62 NREICGDSAYEKGKQVFDVAVYAMGHALHAMHDLCPGRVGLCPMDPDVGTOLLY 121
 DB 387 NREICGDSAYEKGKQVFDVAVYAMGHALHAMHDLCPGRVGLCPMDPDVGTOLLY 446

QY 122 IRNVNFSGIAGNPVTNENGAPGRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERMOWP 181
 DB 447 IRNVNFSGIAGNPVTNENGAPGRYDIYQYQLRNGSAEYKVGISWTDHLHLRIERMOWP 506

QY 182 GSGQQLPRISLPCQPGERKKTVMGACCHCEPCTGYQYQVDRYTKTCYDMPRTEN 241
 DB 507 GSGQQLPRISLPCQPGERKKTVMGACCHCEPCTGYQYQVDRYTKTCYDMPRTEN 566

QY 242 RTSCQPIPIVKLEWDSWAVLPLFLAVVGIAATLFVVVTFVRYNDTPIVKASGRLSYVL 301
 DB 567 RTSCQPIPIVKLEWDSWAVLPLFLAVVGIAATLFVVVTFVRYNDTPIVKASGRLSYVL 626

QY 302 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRSVS 361
DB 627 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRSVS 686
QY 362 APRFISPASQLAITFILISLQLLGICVWFVVDPSHSVVDFDQRTLDRFARGVLKCDIS 421
DB 687 APRFISPASQLAITFILISLQLLGICVWFVVDPSHSVVDFDQRTLDRFARGVLKCDIS 746
QY 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPETFNPAKPIGFTMYTTCIVWLAFIPFPGTS 481
DB 747 DLSLICLLGYSMMLMVTCTVVAIKTRGVPETFNPAKPIGFTMYTTCIVWLAFIPFPGTS 806
QY 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 541
DB 807 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 866
QY 542 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTYVTYTNHAI 584
DB 867 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTYVTYTNHAI 909
RESULT 7
AAR82658
ID AAR82658 standard; protein; 912 AA.
AC AAR82658;
XX
XX
XX 20-DEC-1995 (first entry)
XX Human mGluR4.
XX Metabotropic glutamate receptor 4; mGluR4; stroke; epilepsy;
KW Alzheimer disease; detection; diagnosis; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 588..610
FT /label= TMD-I
FT /note= "transmembrane domain I"
FT 625..645
FT /label= TMD-II
FT /note= "transmembrane domain II"
FT 657..675
FT /label= TMD-III
FT /note= "transmembrane domain III"
FT 699..720
FT /label= TMD-IV
FT /note= "transmembrane domain IV"
FT 751..771
FT /label= TMD-V
FT /note= "transmembrane domain V"
FT 786..807
FT /label= TMD-VI
FT /note= "transmembrane domain VI"
FT 823..847
FT /label= TMD-VII
FT /note= "transmembrane domain VII"
XX
XX W09522609-A2.
XX
XX 24-AUG-1995.
XX
XX 21-FEB-1995; 95WO-GB0000356.
XX
XX 21-FEB-1994; 94GB-00003285.
XX 01-AUG-1994; 94GB-00015532.
XX
XX (WELL) WELLCOME FOUND LTD.
XX
XX Makoff AJ;

DR WPI; 1995-302715/39.
XX N-PSDB; AAT03888.
FT New isolated human metabotropic glutamate receptors - used for detection,
FT diagnosis and therapy of diseases associated with the receptors, eg.
XX stroke, epilepsy and Alzheimer's disease.
XX
XX Claim 2; Page 40-43; 55pp; English.
XX
XX mRNA from the human cerebellum was used to construct a cDNA library. cDNA
CC was amplified by PCR primers (AAT03896-97) based on rat mGluR4 sequences
CC and with the primers given in AAT03898-99 to obtain cDNA encoding human
CC mGluR4
XX
XX Sequence 912 AA;
QY Query Match 96.7%; Score 3004.5; DB 2; Length 912;
DB Best Local Similarity 96.7%; Pred. No. 6e-303;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
QY 3 GVSSSLPRTMT-SGFDRYFSSRTLDDNRRNITWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
DB 330 GAVTILPKRMSVGRGDFRYFSSRTLDDNRRNITWFAEFWEDNFHCKLSRHALKKGSHVKKCT 389
QY 62 NRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMHRDLCPRVGLCPRMDPVDGTQLLKY 121
DB 390 NRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMHRDLCPRVGLCPRMDPVDGTQLLKY 449
QY 122 IRNVNFSGIAGNPVTNENGDAPEGRIYIYQVQLRNGSAEYKVIGSWTDHLHLRIERQWHP 181
DB 450 IRNVNFSGIAGNPVTNENGDAPEGRIYIYQVQLRNGSAEYKVIGSWTDHLHLRIERQWHP 509
QY 182 GSGOQLPRSCSLPCQGERKKTVKGMCCWHCEPCTGYQVQVDRTYCKTCPYDMRPTE 241
DB 510 GSGOQLPRSCSLPCQGERKKTVKGMPCWHCEPCTGYQVQVDRTYCKTCPYDMRPTE 569
QY 242 RTSCQPIPIVKLEWDSWAVLPLFLAVVGIAATLFFVVVTFVRYNDTPIVKASGRELSVYL 301
DB 570 RTGCRPIPIKLEWGSWAVLPLFLAVVGIAATLFFVITFVRYNDTPIVKASGRELSVYL 629
QY 302 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRSVS 361
DB 630 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRSVS 689
QY 362 APRFISPASQLAITFILISLQLLGICVWFVVDPSHSVVDFDQRTLDRFARGVLKCDIS 421
DB 690 APRFISPASQLAITFILISLQLLGICVWFVVDPSHSVVDFDQRTLDRFARGVLKCDIS 749
QY 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPETFNPAKPIGFTMYTTCIVWLAFIPFPGTS 481
DB 750 DLSLICLLGYSMMLMVTCTVVAIKTRGVPETFNPAKPIGFTMYTTCIVWLAFIPFPGTS 809
QY 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 541
DB 810 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 869
QY 542 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTYVTYTNHAI 584
DB 870 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTYVTYTNHAI 912
RESULT 8
AAR23757
ID AAR23757 standard; protein; 912 AA.
XX
XX AAR23757;
XX AC
XX 10-SEP-2002 (first entry)
XX
XX Human metabotropic glutamate (mGluR4) receptor protein.
XX
XX Human; metabotropic glutamate receptor; mGluR4; neurodegeneration;
KW antipsychotic; anticonvulsant; analgesic; antidepressant; antiemetic.

QY 302 LAGIFLCYATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 361
 DB 630 LAGIFLCYATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 689
 QY 362 APRFISPASQALAITFILISLQLLIGICVWFVDPSSHVDFDQDRTLDPRFARGVLKCDIS 421
 DB 690 APRFISPASQALAITFILISLQLLIGICVWFVDPSSHVDFDQDRTLDPRFARGVLKCDIS 749
 QY 422 DLSLICLLGYSMLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAPIPIFFGTS 481
 DB 750 DLSLICLLGYSMLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAPIPIFFGTS 809
 QY 482 QSAKDLXIQTTLTVSVLSASVSLSGLMYPKYIILFHPQONVPRKRSKLVAVTAATM 541
 DB 810 QSAKDLXIQTTLTVSVLSASVSLSGLMYPKYIILFHPQONVPRKRSKLVAVTAATM 869
 QY 542 SNKFTQGNFRPNGEAKSELCELENLEAPALATKQTVVYTNHAI 584
 DB 870 SNKFTQGNFRPNGEAKSELCELENLEAPALATKQTVVYTNHAI 912

RESULT 11

AD58166
 ID ADE58166 standard; protein; 912 AA.

XX AC ADE58166;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein Q14833, SEQ ID NO 4037.

XX KW Human; pain; neuronal tissue; gene therapy;

XX KW spinal segmental nerve injury; chronic constriction injury; CCI;

XX KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX XX (GEMO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX XX Woolf C, D'urso D, Befort K, Costigan M;

XX XX WPI: 2003-268312/26.

XX XX GENBANK; Q14833.

XX PT New composition comprising two or more isolated polypeptides, useful for
 XX PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 912 AA;

Query Match 96.7%; Score 3004.5; DB 7; Length 912;

Best Local Similarity 96.7%; Pred. No. 66-303;

Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 3 GVSSSLPTRMT-SGPDYRFSSRTLNNRRNINWFAEFWEDNPHCKLSRHAKKGSHIKKCT 61

DB 330 GAVTILPKRMSVGRGDRYFSSRTLNNRRNINWFAEFWEDNPHCKLSRHAKKGSHVKKCT 389

QY 62 NRERIGQDSAYEQEGKVQFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLKY 121

DB 390 NRERIGQDSAYEQEGKVQFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLKY 449

QY 122 TRNVNFSGIAGNPVTENGDAPGRYDIYQVLRNGSAEYKVGISWTDLHLRIERMHP 181

DB 450 TRNVNFSGIAGNPVTENGDAPGRYDIYQVLRNGSAEYKVGISWTDLHLRIERMHP 509

QY 182 GSGQQLPRISICSLPCQGERKKTVKGMACCVHCEPCTGYQVODRYTCTCYDMRPTEN 241

DB 510 GSGQQLPRISICSLPCQGERKKTVKGMCCVHCEPCTGYQVODRYTCTCYDMRPTEN 569

QY 242 RTSCQPIPIVKLEWDSMAVLPLFLAVVGGIAATLFFVVTFFVRYNDTPIVKASGRELSTYL 301

DB 570 RTGCRPIPIKLEWGSMAVLPLFLAVVGGIAATLFFVVTFFVRYNDTPIVKASGRELSTYL 629

QY 302 LAGIFLCYATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 361

DB 630 LAGIFLCYATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 689

QY 362 APRFISPASQALAITFILISLQLLIGICVWFVDPSSHVDFDQDRTLDPRFARGVLKCDIS 421

DB 690 APRFISPASQALAITFILISLQLLIGICVWFVDPSSHVDFDQDRTLDPRFARGVLKCDIS 749

QY 422 DLSLICLLGYSMLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAPIPIFFGTS 481

DB 750 DLSLICLLGYSMLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAPIPIFFGTS 809

QY 482 QSAKDLXIQTTLTVSVLSASVSLSGLMYPKYIILFHPQONVPRKRSKLVAVTAATM 541

DB 810 QSAKDLXIQTTLTVSVLSASVSLSGLMYPKYIILFHPQONVPRKRSKLVAVTAATM 869

QY 542 SNKFTQGNFRPNGEAKSELCELENLEAPALATKQTVVYTNHAI 584

DB 870 SNKFTQGNFRPNGEAKSELCELENLEAPALATKQTVVYTNHAI 912

RESULT 12

AD029094

ID AD029094 standard; protein; 912 AA.

XX AC AD029094;

XX DT 29-JUL-2004 (first entry)

XX DE Human novel GPCR GRM4, SEQ ID NO:193.

XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;

transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cystostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic; CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic; viricide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antitumor; antithyroid; antiallergic; anorectic; immunosuppressive; nephroretroic; gene therapy; GPCR modulator; human; receptor.

Homo sapiens.

WO2004040000-A2.

13-MAY-2004.

09-SEP-2003; 2003WO-US028226.

09-SEP-2002; 2002US-0409303P.

09-APR-2003; 2003US-0461329P.

(PRIM-) PRIMAL INC.

Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F, Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

WPI: 2004-390329/36.

N-PSDB; AD029776.

Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

Claim 1; SEQ ID NO 193; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising a mutation in a different GPCR gene of the invention. The probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Seq Sequence 912 AA;

Query Match 96.7%; Score 3004.5; DB 8; Length 912;

Best Local Similarity 96.7%; Pred. No. 6e-303;

Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 3 GVSSSLTRMT-SGFDRYFSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKSGSHKCT 61

DB 330 GAVTILPKRMSVRGFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKSGSHKCT 389

QY 62 NRERIGQDSAYEQSGKVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLY 121

DB 390 NRERIGQDSAYEQSGKVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLY 449

QY 122 IRNVNFSGIAGNPVTNENGDAQGRYDIYQYOLRNGSAEYKVGISWTDHLHLRLERQWP 181

DB 450 IRNVNFSGIAGNPVTNENGDAQGRYDIYQYOLRNGSAEYKVGISWTDHLHLRLERQWP 509

QY 182 GSGQQLPRISICSLPCQPGERKKTVMKMACCWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 241

DB 510 GSGQQLPRISICSLPCQPGERKKTVMKMACCWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 569

QY 242 RTSCQPIPIVKLEWDSWPAVLPLFLAVVGTAAATLVVVVTVFRVYNDTPIVKSAGRELSYVL 301

DB 570 RTGCRPIPIIKLEWDSWPAVLPLFLAVVGTAAATLVVVVTVFRVYNDTPIVKSAGRELSYVL 629

QY 302 LAGIFLCVATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361

DB 630 LAGIFLCVATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 689

QY 362 APREISPASQLAITFIIISLQLGICVWFVVDPSHVVDFQDQRTLDPRFARGVCLKDIS 421

DB 690 APREISPASQLAITFIIISLQLGICVWFVVDPSHVVDFQDQRTLDPRFARGVCLKDIS 749

QY 422 DLSLICLLGYSMILMVTCTVYAIKTRGVPEFNEAKDPIGFTMYTTCIVWLAFIPIFGTS 481

DB 750 DLSLICLLGYSMILMVTCTVYAIKTRGVPEFNEAKDPIGFTMYTTCIVWLAFIPIFGTS 809

QY 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVIIILFHPQONVPRKRSLSKAVVTAATM 541

DB 810 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVIIILFHPQONVPRKRSLSKAVVTAATM 589

QY 542 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTYVTVYTNHAI 584

DB 870 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTYVTVYTNHAI 912

RESULT 13

ADQ89114

ID ADQ89114 standard; protein; 912 AA.

XX AC ADQ89114;

XX DT 21-OCT-2004 (first entry)

XX DE Human urological disorder related protein 115 SEQ:66.

XX KW urological disorder; uropathic; cytostatic; urinary incontinence;

XX KW benign prostatic hyperplasia; human.

XX OS Homo sapiens.

XX FN WO2004065576-A2.

XX PD 05-AUG-2004.

XX PF 14-JAN-2004; 2004WO-US0000750.

XX PR 15-JAN-2003; 2003US-0440318P.

XX PR 04-FEB-2003; 2003US-0444783P.

XX PR 27-MAR-2003; 2003US-0457901P.

XX PR 08-MAY-2003; 2003US-0468775P.

XX PR 19-MAY-2003; 2003US-0471614P.

PR 16-JUN-2003; 2003US-0478742P.
 PR 18-JUL-2003; 2003US-0488529P.
 PR 30-JUL-2003; 2003US-0491156P.
 PR 02-SEP-2003; 2003US-0499594P.
 PR 26-SEP-2003; 2003US-0506332P.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Karicheti V, Silos-Santiago I, Eliasof SD;
 XX WPI; 2004-562167/54.
 DR N-PSDB; ADQ89113.
 XX Use of polypeptides related to urological disorders, e.g. 44390, 54181,
 PT 211 or for identifying a compound capable of treating a urological
 PT disorder or identifying and treating a subject having a urological
 PT disorder.
 XX Claim 1; SEQ ID NO 66; 542pp; English.
 PS The present invention describes the use of polypeptides related to
 CC urological disorders for identifying a compound capable of treating a
 CC urological disorder, identifying a subject having a urological disorder,
 CC or treating a subject having a urological disorder. Also described: (1) a
 CC method for identifying a compound capable of treating a urological
 CC disorder; (2) a method for identifying a subject having a urological
 CC disorder; and (3) a method for treating a subject having a urological
 CC disorder. The compound has uropathic and cytostatic activities. The
 CC polypeptides related to urological disorders are useful for identifying a
 CC compound capable of treating a urological disorder, identifying a subject
 CC having a urological disorder, or treating a subject having a urological
 CC disorder. Disorders include urinary incontinence and benign prostatic
 CC hyperplasia. The present sequence represents a human urological disorder
 CC related protein, which is used in the exemplification of the present
 CC invention.
 XX Sequence 912 AA;
 SQ
 Query Match 96.7%; Score 3004.5; DB 8; Length 912;
 Best Local Similarity 96.7%; Pred. No. 6e-303;
 Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
 QY 3 GVSSSLPTMT-SGPDYFSSRTLDNRRNIWFAEFWEDNFHCKLSRHALKGSHVKCT 61
 DB 330 GAVTILPKMSVGRGDFRYSRTLDNRRNIWFAEFWEDNFHCKLSRHALKGSHVKCT 389
 QY 62 NRERIGDSAYEQEGKQVFDVAVYAMGHAMHREDLCPGRVGLCPRPMDPVDGTQLKY 121
 DB 390 NRERIGDSAYEQEGKQVFDVAVYAMGHAMHREDLCPGRVGLCPRPMDPVDGTQLKY 449
 QY 122 IRNVNFGSIAGNPVTNENGDAFGRVDIYQYQLRNGSAEYKVIKGTWTDHLHLRIERMOWP 181
 DB 450 IRNVNFGSIAGNPVTNENGDAFGRVDIYQYQLRNGSAEYKVIKGTWTDHLHLRIERMOWP 509
 QY 182 GSGQQLPRISCSLPCQPGSRKTKTKGMPCCWCEPCTGYQYQVDRYTKTCPYDMRPTEN 241
 DB 510 GSGQQLPRISCSLPCQPGSRKTKTKGMPCCWCEPCTGYQYQVDRYTKTCPYDMRPTEN 569
 QY 242 RYSCQPIPIKLEWSPWAVLPLFLAVGIAATLFVVTFFVYNDPPIVKASGRELSYVL 301
 DB 570 RYTCRPIPIKLEWSPWAVLPLFLAVGIAATLFVVTFFVYNDPPIVKASGRELSYVL 629
 QY 302 LAGIFLCYATTFILMIAEPDLGTCSLRRIIFLGMSISYAALLTKTNRIYRIEQQKRSYS 361
 DB 630 LAGIFLCYATTFILMIAEPDLGTCSLRRIIFLGMSISYAALLTKTNRIYRIEQQKRSYS 689
 QY 362 APRFISPAQLAITFLISLQLGICVWFVDPSPSVVDFOQRTLDPRFARGVLKCDIS 421
 DB 690 APRFISPAQLAITFLISLQLGICVWFVDPSPSVVDFOQRTLDPRFARGVLKCDIS 749
 QY 422 DLSLICLLGYSMMLAVTCTVYAIKTRGVPTETNEAKPIGFTMYTTCIVMLAIPFPFGTS 481
 DB 750 DLSLICLLGYSMMLAVTCTVYAIKTRGVPTETNEAKPIGFTMYTTCIVMLAIPFPFGTS 809
 QY 482 QSADKLYTQTTLTVSVLSASVSIGMLYMPKVYIILFHPQONVPRKRSKXAVVTAATM 541
 DB 810 QSADKLYTQTTLTVSVLSASVSIGMLYMPKVYIILFHPQONVPRKRSKXAVVTAATM 869
 QY 542 SNKFTQKGNFRNGEAKSELCELENLETPALATKQTVVYTNHAI 584
 DB 870 SNKFTQKGNFRNGEAKSELCELENLETPALATKQTVVYTNHAI 912
 RESULT 14
 AAR72092
 ID AAR72092 standard; protein; 912 AA.
 XX AAR72092;
 AC 25-MAR-2003 (revised)
 DT 26-SEP-1995 (first entry)
 XX Human mGluR4.
 DE Human metabotropic glutamate receptor subtype 4; mGluR4; hmGluR4;
 KW signal transducer.
 XX Homo sapiens.
 OS WO9508627-A1.
 PN 30-MAR-1995.
 PD 07-SEP-1994; 94WO-EP002991.
 PF 20-SEP-1993; 93EP-00810663.
 PR 19-AUG-1994; 94GB-00016553.
 XX (CIBA) CIBA GEIGY AG.
 PA Flor PJ, Kuhn R, Lindauer K, Puettner I, Knoepfel T;
 PI WPI; 1995-139596/18.
 DR N-PSDB; AQ89342.
 XX Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and 7 - also
 PT corresp. DNA and antibodies, useful for identifying cpds. which modulate
 PT signal transduction activity.
 XX Claim 2; Page 44-48; 110pp; English.
 PS Human metabotropic glutamate receptor subtype 4 (hmGluR4) cDNA clones
 CC were isolated from a cerebellum cDNA library using a rat mGluR4 probe.
 CC Clone cMR20 lacked the 5' end of the hmGluR4 gene. PCR using human
 CC genomic or brain cDNA as template was used to obtain a complete gene
 CC sequence (given in AQ89342) encoding hmGluR4 (AAR72092). Recombinant
 CC hmGluR4 was produced in mammalian cells. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX Sequence 912 AA;
 SQ
 Query Match 96.6%; Score 3001.5; DB 2; Length 912;
 Best Local Similarity 96.6%; Pred. No. 1.2e-302;
 Matches 563; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
 QY 3 GVSSSLPTMT-SGPDYFSSRTLDNRRNIWFAEFWEDNFHCKLSRHALKGSHVKCT 61
 DB 330 GAVTILPKMSVGRGDFRYSRTLDNRRNIWFAEFWEDNFHCKLSRHALKGSHVKCT 389
 QY 62 NRERIGDSAYEQEGKQVFDVAVYAMGHAMHREDLCPGRVGLCPRPMDPVDGTQLKY 121
 DB 390 NRERIGDSAYEQEGKQVFDVAVYAMGHAMHREDLCPGRVGLCPRPMDPVDGTQLKY 449
 QY 122 IRNVNFGSIAGNPVTNENGDAFGRVDIYQYQLRNGSAEYKVIKGTWTDHLHLRIERMOWP 181
 DB 450 IRNVNFGSIAGNPVTNENGDAFGRVDIYQYQLRNGSAEYKVIKGTWTDHLHLRIERMOWP 509

QY 182 GSGQQLPRISICSLPCQGERKKTVMKMACCHCEBCTGYQVQVDRYCTCTCPYDMRPTE 241
DB 510 GSGQQLPRISICSLPCQGERKKTVMKMACCHCEBCTGYQVQVDRYCTCTCPYDMRPTE 569
QY 242 RTSCQPIPIVLEWDSWAVLPLFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 301
DB 570 RTGCRPIPIKLEWGSWAVLPLFLAVVGIATLFFVITFVRYNDTPIVKASGRELSYVL 629
QY 302 LAGIFLCVATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 361
DB 630 LAGIFLCVATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 689
QY 362 APRFISPASQALAITFILISLQLGICVWFVVDPSHVVDFDQRTLDPFRFARGVLKCDIS 421
DB 690 APRFISPASQALAITFILISLQLGICVWFVVDPSHVVDFDQRTLDPFRFARGVLKCDIS 749
QY 422 DLSLICLLGYSMLLMVTCTVVAIKTRGVPETFNPAKPIGFTMYTTCIVWLAFIPIFFGTS 481
DB 750 DLSLICLLGYSMLLMVTCTVVAIKTRGVPETFNPAKPIGFTMYTTCIVWLAFIPIFFGTS 809
QY 482 QSADKLYIQTITTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSLSKAVVTAATM 541
DB 810 QSADKLYIQTITTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSLSKAVVTAATM 869
QY 542 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTVVYTNHAI 584
DB 870 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTVVYTNHAI 912

RESULT 15

ADRO8623

ID ADRO8623 standard; protein; 591 AA.

XX AC ADRO8623;

XX DT 04-NOV-2004 (first entry)

XX DE Human protein useful for treating neurological disease Seq 2129.

XX KW human; oligo-capping method; diagnostic marker; gene therapy;
XX KW osteoporosis; neurological disease; Alzheimer's disease;
XX KW Parkinson's disease; dementia; short memory; cancer;
XX KW sense or motor function; emotional reaction; fear response; panic;
XX KW osteopathic; neuroprotective; neurotropic; antiparkinsonian; cytostatic;
XX KW tranquiliser.

XX OS Homo sapiens.

XX PN EP1447413-A2.

XX PD 18-AUG-2004.

XX PF 12-FEB-2004; 2004EP-00003145.

XX PR 14-FEB-2003; 2003JP-00102207.

XX PR 09-MAY-2003; 2003JP-00131452.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
XX PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX DR WPI; 2004-583265/57.
XX DR N-PSDB; ADRO6667.

XX PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
XX PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX PS Claim 1; SEQ ID NO 2129; 2686pp; English.

XX CC This invention relates to novel, isolated full length human cDNA
XX CC molecules and the encoded proteins thereof. Specifically, it refers to

CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunoassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, neurotropic, antiparkinsonian,
CC cyostatic and tranquiliser activities. This polypeptide is a protein
CC encoded by a full length human cDNA sequence of the invention. NOTE: This
CC sequence is not given in the sequence listing of the specification but
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
CC office.

XX SQ Sequence 591 AA;

Query Match 93.7%; Score 2912.5; DB 8; Length 591;

Best Local Similarity 96.1%; Pred. No. 1.2e-293;

Matches 545; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 3 GVSSSLPRTMT-SGFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKCT 61

DB 22 GAVTILPKRMSVRGFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKCT 81

QY 62 NRERIGQDSAYEOEGKVQFVIDAVYANGHALHAMHRDLCPGRVGLCPMPDPVDTQLLY 121

DB 82 NRERIGQDSAYEOEGKVQFVIDAVYANGHALHAMHRDLCPGRVGLCPMPDPVDTQLLY 141

QY 122 IRNVNFGSIAGNPVTFNENGDAPEGYDIYQVQLNGSAEYKVGISWTDHLHLRERQWP 181

DB 142 IRNVNFGSIAGNPVTFNENGDAPEGYDIYQVQLNGSAEYKVGISWTDHLHLRERQWP 201

QY 182 GSGQQLPRISICSLPCQGERKKTVMKMACCHCEBCTGYQVQVDRYCTCTCPYDMRPTE 241

DB 202 GSGQQLPRISICSLPCQGERKKTVMKMACCHCEBCTGYQVQVDRYCTCTCPYDMRPTE 261

QY 242 RTSCQPIPIVLEWDSWAVLPLFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 301

DB 262 RTGCRPIPIKLEWGSWAVLPLFLAVVGIATLFFVITFVRYNDTPIVKASGRELSYVL 321

QY 302 LAGIFLCVATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 361

DB 322 LAGIFLCVATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 381

QY 362 APRFISPASQALAITFILISLQLGICVWFVVDPSHVVDFDQRTLDPFRFARGVLKCDIS 421

DB 382 APRFISPASQALAITFILISLQLGICVWFVVDPSHVVDFDQRTLDPFRFARGVLKCDIS 441

QY 422 DLSLICLLGYSMLLMVTCTVVAIKTRGVPETFNPAKPIGFTMYTTCIVWLAFIPIFFGTS 481

DB 442 DLSLICLLGYSMLLMVTCTVVAIKTRGVPETFNPAKPIGFTMYTTCIVWLAFIPIFFGTS 501

QY 482 QSADKLYIQTITTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSLSKAVVTAATM 541

DB 502 QSADKLYIQTITTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSLSKAVVTAATM 561

QY 542 SNKFTQKGNFRPNGEAKSELCELENLETP 568

DB 562 SNKFTQKGNFRPNGEAKSELCELENLETP 588

Search completed: June 17, 2005, 18:14:23
Job time : 173 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 17, 2005, 18:19:18 ; Search time 315.5 Seconds

(without alignments)

5696.982 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 3303

Sequence: 1 atgcacagggtatcatc.....acacacacatgcatctatg 1755

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cpn2.1/USPTO spool_p/US10828332/runat 17062005 171336 24951/app query.fasta_1.1927
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10828332 @CN 1 1 354 @runat 17062005 171336 24951 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3050.5	92.4	912	1 MGR4 RAT	P31423 rattus norv
2	2004.5	91.0	912	1 MGR4_HUMAN	Q14833 homo sapien
3	2752.5	83.3	796	2 Q62MQ2	Q62mq2 homo sapien
4	2732	82.7	983	2 Q62916	Q62916 rattus norv
5	2546.5	77.1	832	2 Q68EF4	Q68ef4 mus musculus
6	2377	72.0	908	1 MGR8 HUMAN	O00222 homo sapien
7	2377	72.0	908	2 Q6B964	Q6b964 mus musculus
8	2371	71.8	908	1 MGR8 RAT	P70579 rattus norv
9	2336	70.7	908	1 MGR8_MOUSE	P47743 mus musculus
10	2219	67.2	915	1 MGR7_HUMAN	Q14831 homo sapien
11	2214	67.0	915	2 Q68ED2	Q68ed2 mus musculus
12	2210	66.9	915	1 MGR7 RAT	P35400 rattus norv
13	2189	66.3	906	2 Q8NFS2	Q8nfs2 homo sapien
14	2189	66.3	911	2 Q8NFS3	Q8nfs3 homo sapien
15	2189	66.3	924	2 Q8NFS4	Q8nfs4 homo sapien
16	2111.5	63.9	551	2 Q9PWQ0	Q9pwq0 fugu rubrip

17	2069.5	62.7	680	2 Q76MR0	Q76mr0 poephila gu
18	2054	62.2	877	1 MGR6_HUMAN	Q15303 homo sapien
19	2045.5	61.9	868	1 MGR6_HUMAN	Q86314 oryctolagus
20	2026.5	61.4	871	1 MGR6 RAT	P35349 rattus norv
21	1967.5	59.6	546	2 Q8CFQ7	Q8cfq7 mus musculus
22	1962.5	59.4	977	2 Q9PWE1	Q9pwe1 ictalurus p
23	1855	56.2	620	2 Q76E43	Q76e43 poephila gu
24	1284.5	38.9	1520	2 Q8NHA9	Q8nha9 homo sapien
25	1240.5	37.6	976	1 MGR DROME	P91685 drosophila
26	1223.5	37.0	780	2 Q7KQ59	Q7kq59 drosophila
27	1223.5	37.0	1073	2 Q7OGQ8	Q7ogq8 drosophila
28	1223.5	37.0	1226	2 Q9V4U3	Q9v4u3 drosophila
29	1223.5	37.0	1264	2 Q9V4U4	Q9v4u4 drosophila
30	1181	35.8	933	2 Q75QW7	Q75qw7 apis mellif
31	1179	35.7	843	2 Q6S738	Q6s738 apis mellif
32	1171.5	35.5	872	1 MGR2 RAT	P31421 rattus norv
33	1155.5	35.0	877	1 MGR3_HUMAN	Q14832 homo sapien
34	1155.5	35.0	879	1 MGR3_MOUSE	Q9GY82 mus musculus
35	1155.5	35.0	879	2 Q86YG6	Q86yg6 homo sapien
36	1152.5	34.9	879	1 MGR3 RAT	P31422 rattus norv
37	1150.5	34.8	872	1 MGR2_HUMAN	Q14416 homo sapien
38	1148.5	34.8	877	2 Q8TBH9	Q8tbh9 homo sapien
39	1148.5	34.8	1040	2 Q75QW6	Q75qw6 apis mellif
40	1129	34.2	1194	1 MGR1_HUMAN	Q13255 homo sapien
41	1123	34.0	942	2 Q6J164	Q6j164 homo sapien
42	1123	34.0	1212	1 MGR5_HUMAN	P41594 homo sapien
43	1122	34.0	1156	2 Q98UC6	Q98uc6 gallus gall
44	1122	34.0	1188	2 Q98UC5	Q98uc5 gallus gall
45	1122	34.0	1199	1 MGR1 RAT	P23385 rattus norv

ALIGNMENTS

RESULT 1

MGR4 RAT
ID MGR4 RAT STANDARD; PRT; 912 AA.
AC P31423;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 4 precursor (mGluR4).
GN Name=Gm4; Synonyms=Gprcid, Mglur4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93332699; PubMed=8338667;
RA O'Hara P.J., Sheppard P.O., Thoenes H., Venezia D., Haldeman B.A.,
RA McGrane V., Houamed K.M., Thomsen C., Gilbert T.L., Mulvihill E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
RN [3]
RP INTERACTION WITH PRKCAP.
RX MEDLINE=20571397; PubMed=1112333;
RA El Far O., Afras J., Wischmeyer E., Nehring R.B., Karschin A.,
RA Betz H.;
RT "Interaction of the C-terminal tail region of the metabotropic
glutamate receptor 7 with the protein kinase C substrate PICK1.";
RL Eur. J. Neurosci. 12:4215-4221(2000).
CC -!- FUNCTION: Receptor for glutamate. The activity of this receptor is
mediated by a G-protein that inhibits adenylyl cyclase activity.
CC -!- SUBUNIT: Interacts with PRKCAP.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Is widely distributed in the CNS. Predominant
 CC expression is seen in the granule cells of the cerebellum.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC -----

DR EMBL; M92077; -; NOT ANNOTATED_CD.
 DR EMBL; M90518; AAA93190.1; -.
 DR PIR; JH0563; JH0563.
 DR HSSP; P23385; LEWK.
 DR RGD; 2745; Grm4.
 DR InterPro; IPR001028; ANF receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR000162; Mtblu_receptor.
 DR InterPro; IPR001786; Mtblu_receptor4.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF receptor; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 DR G-protein coupled receptor; Glycoprotein; Multigene family; Signal;
 KW Transmembrane.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 912 Metabotropic glutamate receptor 4.
 FT DOMAIN 33 587 Extracellular (Potential).
 FT TRANSMEM 588 610 1 (Potential).
 FT DOMAIN 611 624 Cytoplasmic (Potential).
 FT TRANSMEM 625 645 2 (Potential).
 FT DOMAIN 646 656 Extracellular (Potential).
 FT TRANSMEM 657 675 3 (Potential).
 FT DOMAIN 676 699 Cytoplasmic (Potential).
 FT TRANSMEM 700 720 4 (Potential).
 FT DOMAIN 721 750 Extracellular (Potential).
 FT TRANSMEM 751 772 5 (Potential).
 FT DOMAIN 773 785 Cytoplasmic (Potential).
 FT TRANSMEM 786 808 6 (Potential).
 FT DOMAIN 809 821 Extracellular (Potential).
 FT TRANSMEM 822 847 7 (Potential).
 FT DOMAIN 848 912 Cytoplasmic (Potential).
 FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 301 301 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 454 454 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 569 569 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 124 124 Q -> R (in Ref. 2).
 SQ SEQUENCE 912 AA; 101818 MW; 336430EF19B48577 CRC64;

Alignment Scores:

Pred. No.: 5,846-174 Length: 912
 Score: 3050.50 Matches: 575
 Percent Similarity: 98.97% Conservative: 2
 Best Local Similarity: 98.63% Mismatches: 5
 Query Match: 92.36% Indels: 1
 DB: 1 Gaps: 1

US-10-828-332-6 (1-1755) x MGR4_RAT (1-912)

QY 7 GGGGTATCATCATCTTTGCCACGAGGATGACA---TCAGGGTTCGACCGATACCTCTCC 63
 DB 330 GlyAlaValThrLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
 QY 64 AGCCGACGCTGGACACACAGCGGCAACATCTGTTTGGCGAGTCTGGGAGGACAAAC 123
 DB 350 SerArgThrLeuAspAsnAsnArgAsnIleTyrPheAlaGluPheTyrGluAspAsn 369

QY 124 TTCCATTGCAAGTTGAGCGCCACGCGCTCAAGAAAGGAAGCCACATCAAGAAGTGACC 183
 DB 370 PheHisCysIysLeuSerArgHisAlaLeuIysGlySerHisIleLeuIysCysThr 389
 QY 184 AACCGAGAGCGCATCGGGCAGGACTCGCCCTATAGCAGGAGGGGAAGTGCAGTCTGT 243
 DB 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
 QY 244 ATTGACGCTGTAGCGCATGGGCGCACGCGCTGCACGCCATGCACCGTGCAGTGTGTC 303
 DB 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 QY 304 GGGCGGTAGGACTCTGCCCTCGCATGGACCCCGTGGATGGCACCCAGCTCTTAAGTAC 363
 DB 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuIysTyr 449
 QY 364 ATCAGGAACGTCACCTCTTCAGGCATTTCGGGGAAACCTGTAACTTCAATGAAACGGA 423
 DB 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 GACCGACGGGGCGCTAGGACATCTACAGTACCAACTGCCAATGGCTCGGCGGATAC 483
 DB 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 489
 QY 484 AAGGTCTATCGGCTCGTGACAGACACCTGCACCTCAGAATAGAGCGGATGCAGTGGCCA 543
 DB 490 LysValIleGlySerThrAspHisLeuHisLeuArgIleGluArgMetGlnTyrPro 509
 QY 544 GGGAGTGGCCACGACGCTGCCGCGCTCCATCTGCAGTCTGCCCTCCAGCCCGGGAGCGA 603
 DB 510 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAAGCTGTGAAGGCGATGGCTTGTCTGGCGACTGCGAGCCCTGCACCGGTACCAG 663
 DB 530 LysIysThrValIysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATGCGGCCCCACAGAGAAC 723
 DB 550 TyrGlnValAspArgTyrThrCysIysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CGCAGAGCTGCCAGCCATCCCATCGTCAAGTTGAGTGGAGTGGAGTGGCGCGGTG 783
 DB 570 ArgThrSerCysGlnProIleValIysLeuGluTyrAspSerProTyrAlaVal 589
 QY 784 CTGCCCTCTCTCTGGCGGTGGTGGCATCGCCCGCAGCTGTTGCTGGTGCCTCAGCTTT 843
 DB 590 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValValThrPhe 609
 QY 844 GTGGCTACCAACGATACCCCATCGTCAAGGCTCGGGCCGGGAACCTGAGCTAGTGTCTG 903
 DB 610 ValArgTyrAsnAspThrProIleValIysAlaSerGlyArgGluLeuSerTyrValLeu 629
 QY 904 CTGGCGGCGCATCTTTCTGTGTACGCCACTACCTTCCTCATGATCGCAGACCGGACCTG 963
 DB 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
 QY 964 GGGACCTGTTCGCTCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGCTACGCGGCC 1023
 DB 650 GlyThrCysSerLeuArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
 QY 1024 CTGCTGACCAAGACCAACCGCATTTTACCGCATCTTTGAGCAGGGCAACGCTCGGTCAGT 1083
 DB 670 LeuLeuThrIysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
 QY 1084 GCCCGCGCTTTTCATCAGCCCGGCTCGCAGCTGGCCATCACCTTCATCTCTCCCTG 1143
 DB 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 709
 QY 1144 CAGCTGCTCGGCATCTGGGTGTGTGTTGTTGTTGACCCCTCCCACTCGGTGGTGCAGTTC 1203
 DB 710 GlnLeuLeuGlyIleCysValTyrPheValValAspProSerHisSerValValAspPhe 729

QY 1204 CAGGACCAACGACACTTGCACCCCGCTTTCAGGGCGTCTCAAGTCCGACATCTCG 1263
 DB 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
 QY 1264 GACCTCTCCCTCATCTGCTGCTGGCTACAGCATGCTGCTGATGGTCACTGTACTGTG 1323
 DB 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
 QY 1324 TAGCCCATCAAGACCCGAGCGGTGCGCGAGACTTCAACGAGGCCAAGCCCATCGGCTTC 1383
 DB 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
 QY 1384 ACATGTTACACCACTGCTGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
 DB 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 809
 QY 1444 CAGTACGCGCACAAGCTGTACATCCAGACACACACTCACGCTTCCTGAGTGTGAGC 1503
 DB 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 829
 QY 1504 GTTTCAGTCTCCCTGGGATGCTTACATGCCAAAGTCTACATCATCTCTTCCACCCG 1563
 DB 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
 QY 1564 GAGCAGAACTGCCCAAGCGCGAGCGCAGCTCTCAAGCGCTGCTACCGCCGCCACCATG 1623
 DB 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 869
 QY 1624 TCCACAAGTTCACAGAGGCGCACTTCAGSCCAATGGGAGGCAAGCAAAATCAGAGCTG 1683
 DB 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
 QY 1684 TGTGAGAACTGGAGACCCAGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1743
 DB 890 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
 QY 1744 CATGCCATC 1752
 DB 910 HisAlaIle 912

RESULT 2
 MGR4 HUMAN
 ID MGR4_HUMAN STANDARD; PRT; 912 AA.
 AC Q14833;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Metabotropic glutamate receptor 4 precursor (mGluR4).
 GN Name=GRM4; Synonyms=GPRC1D, MGLUR4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96346635; PubMed=8738157; DOI=10.1016/0169-328X(95)00321-1;
 RA Makoff A., Leichuk R., Oker M., Harrington K., Emson P.;
 RT "Molecular characterization and localization of human metabotropic
 glutamate receptor type 4.";
 RL Brain Res. Mol. Brain Res. 37:239-248 (1996).
 RP [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98141892; PubMed=9473604; DOI=10.1016/S0169-328X(97)00277-5;
 RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
 RA Rosbeck P.R. Jr., Johnson B.G., Schoep D.D., Belagaje R.M.;
 RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
 molecular cloning, functional expression, and comparison of
 pharmacological properties in RGT cells.";
 RL Brain Res. Mol. Brain Res. 53:88-97 (1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RX MEDLINE=95342351; PubMed=7617140; DOI=10.1016/0028-3908(94)00149-M;
 RA Flor P.J., Lukic S., Rueegg D., Leonhardt T., Knoepfel T., Kuhn R.;
 RT "Molecular cloning, functional expression and pharmacological
 characterization of the human metabotropic glutamate receptor type
 4.";
 RL Neuropharmacology 34:149-155 (1995).
 RN [4]
 RP VARIANT IIS-797.
 RX MEDLINE=21416233; PubMed=11525421;
 RA Ohtsuki T., Toru M., Arinami T.;
 RT "Mutation screening of the metabotropic glutamate receptor mGluR4
 (GRM4) gene in patients with schizophrenia.";
 RL Psychiatr. Genet. 11:79-83 (2001).
 CC -!- FUNCTION: Receptor for glutamate. The activity of this receptor is
 mediated by a G-protein that inhibits adenylyl cyclase activity.
 CC -!- SUBUNIT: Interacts with PRKCAP (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Strongly expressed in the cerebellum.
 CC Expressed at low levels in hippocampus, hypothalamus and thalamus.
 CC No expression detected in liver.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X80818; CAA56784.1; -;
 CC EMBL; U92457; AB51762.1; -;
 CC HSSP; P23385; LEWK.
 CC Genew; HGNC:4596; GRM4.
 CC MIM; 604100; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . . ; TAS.
 CC GO; GO:0007194; P:negative regulation of adenylyl cyclase ac. . . ; TAS.
 CC GO; GO:0007268; P:synaptic transmission; TAS.
 CC InterPro; IPR001828; ANF receptor.
 CC InterPro; IPR000337; GPCR_Mgr.
 CC InterPro; IPR000162; Mglu_receptor.
 CC InterPro; IPR001786; Mglu_receptor4.
 CC Pfam; PF00003; 7tm_3; 1.
 CC Pfam; PF01094; ANF receptor; 1.
 CC PRINTS; PR00248; GPCR_MGR.
 CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 CC PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 CC G-protein coupled receptor; Glycoprotein; Multigene family;
 KW Polymorphism; Signal; Transmembrane.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 912 Metabotropic glutamate receptor 4.
 FT DOMAIN 33 587 Extracellular (Potential).
 FT TRANSMEM 588 610 1 (Potential).
 FT DOMAIN 611 624 Cytoplasmic (Potential).
 FT TRANSMEM 625 645 2 (Potential).
 FT DOMAIN 646 656 Extracellular (Potential).
 FT TRANSMEM 657 675 3 (Potential).
 FT DOMAIN 676 699 Cytoplasmic (Potential).
 FT TRANSMEM 700 720 4 (Potential).
 FT DOMAIN 721 750 Extracellular (Potential).
 FT TRANSMEM 751 772 5 (Potential).
 FT DOMAIN 773 785 Cytoplasmic (Potential).
 FT TRANSMEM 786 808 6 (Potential).
 FT DOMAIN 809 821 Extracellular (Potential).
 FT TRANSMEM 822 847 7 (Potential).
 FT DOMAIN 848 912 Cytoplasmic (Potential).
 FT CARBOHYD 98 98 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 301 301 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 454 454 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 484 484 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 569 569 N-linked (GlcNAc...) (Potential).
 FT VARIANT 797 797 V -> I.
 FT /FTID=VAR_012992.
 SQ SEQUENCE 912 AA; 101867 MW; 4A2F36E63A2EAF5A CRC64;

Alignment Scores:
 Pred. No.: 3,27e-171 Length: 912
 Score: 3004.50 Matches: 564
 Percent Similarity: 97.77% Conservative: 6
 Best Local Similarity: 96.74% Mismatches: 12
 Query Match: 90.96% Indels: 1
 DB: 1 Gaps: 1

US-10-828-332-6 (1-1755) x MGR4_HUMAN (1-912)

QY	7	GGGGTATCATCATCTTTGTCACAGGAGGATGACA---TCAGGGTTTCGACCGCATCTCTCC	63
Db	330	GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer	349
QY	64	AGCCGACGCTGGCAACAACAGGCGCAACATCTGTTTGGCGAGTTCGGGAGGACAAC	123
Db	350	SerArgThrLeuAspAsnAsnArgAsnIleThrPheAlaGluPheTrpGluAspAsn	369
QY	124	TTCCATTGCAAGTTGAGCCGCCACCGCTCAAGAAAGGGAAGCCACATCAAGAAGTGACC	183
Db	370	PheHisCysLeuSerArgHisAlaLeuLysLysGlySerHisValLysLysCysThr	389
QY	184	AACCGAGCGGATCGGGAGAGCTCGCGCTATGAGCAGAGGAGGGAAGGTGAGTTCGTG	243
Db	390	AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal	409
QY	244	ATTGACGCTGTACGCCATGGCCACGCGTGCACGCGCATGCGACCGTGACTGTGTC	303
Db	410	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	429
QY	304	GGCCCGTAGGACTTCGCCCTCGCATGGACCCCGTGGATGGCACCGACTGCTTAAGTAC	363
Db	430	GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr	449
QY	364	ATCAGGAACGTCAATCTTCAGGCATTCGGGGAAACCTGTAACTTCATAGAGAACGGA	423
Db	450	IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly	469
QY	424	GAGCAGCGGGCGGTACGACATCTACAGTACCACTGCGCAATGGCTCGCGCGAGTAC	483
Db	470	AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr	489
QY	484	AAGGTATCATCGGCTCGTGACAGACACCTTCACCTCAGAATAGAGCGGATGAGTGCCA	543
Db	490	LysValIleGlySerTrpThrAspHisLeuHisLeuArgGlyLeuArgMetHisTrpPro	509
QY	544	GGGAGTGCCAGCAGCTCGCGCTCCATCTGTCAGTCTGCCCTGCGCCCGGGAGCGGA	603
Db	510	GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg	529
QY	604	AGAGACTGTCAAGGGATGCTTCTGCTGGCACTGGAGCCCTGACCGGGTACCCAG	663
Db	530	LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln	549
QY	664	TACCAAGTGGACCGCTACACCTGTGAAGACCTGCCCCCTACGATCGCGCCACAGAGAAC	723
Db	550	TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn	569
QY	724	CGCAGAGCTGCACGCCATCCCCATCGTCAAGTTGGAGTGGAGCTCGCGTGGCCGTG	783
Db	570	ArgThrGlyCysArgProIleProIleIleLysLeuGluTyrGlySerProTrpAlaVal	589
QY	784	CTGCCCTCTCTCTCGCGTGTGGGCACTCGCGCAGCTGTTCTGCTGGTTCACGTTT	843
Db	590	LeuProLeuPheLeuAlaValGlyIleAlaIleAlaThrLeuPheValIleThrPhe	609
QY	844	GTGCGCTACAAGATACCCCCATCGTCAAGGCGCTCGGGCGGGAACTGAGCTACGTGCTG	903

Db	610	ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu	629
QY	904	CTGGCGGGCATCTTCTGTCTGCTAGCCACTACCTCTCTCATGATCGAGAGCCGACCTG	963
Db	630	LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu	649
QY	964	GGGACCTGTTCTGCTCCGCGCATCTTCTAGGGCTCGGCATAGCATCAGCTACGCGGCC	1023
Db	650	GlyThrCysSerLeuArgGlyIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla	669
QY	1024	CTGCTGACCAAGAACCAACCGCATTTACCGCATCTTTGAGCAGGGCAACCGTTCGTCAGT	1083
Db	670	LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer	689
QY	1084	GCCCCGGTTTCATCAGCCCGCTCGCAGCTGGCCATCACCTTCATCTCTCTCTCTCTG	1143
Db	690	AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu	709
QY	1144	CAGCTGCTCGGCATCTCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1203
Db	710	GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe	729
QY	1204	CAGACCAACGACCATTTGACCCCGCTTTCAGGGGGCTGCTCAAGTGGCAGCATCTCG	1263
Db	730	GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer	749
QY	1264	GACCTGCTCCCTCATCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1323
Db	750	AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal	769
QY	1324	TACCCCATCAAGACCCCGAGCGCTCGCCGAGACCTTCAACGAGGGCAAGCCCATCGGCTTC	1383
Db	770	TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe	789
QY	1384	ACCATGTACACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1443
Db	790	ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer	809
QY	1444	CAGTCAGCGCAGCTGTATCATCCAGACCAACCATCAGCTGCTGCTGCTGCTGCTGCTG	1503
Db	810	GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer	829
QY	1504	GCTTCAGTGTCTCTGGGGATGCTCTACATGCCCAAGTCTACATCATCTCTCTCCACCCG	1563
Db	830	AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro	849
QY	1564	GAGCAGAACGTGCCAACGACGACGCTCTCAAGCCGTGCTGCTGCTGCTGCTGCTGCTG	1623
Db	850	GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet	869
QY	1624	TCCAAACAGTTTCACACAGAGGGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG	1683
Db	870	SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu	889
QY	1684	TGTGAGAACCTTGGAGACCCCGAGCGCTGCTACCAAAACAGACCTACGTCACCTACCAAC	1743
Db	890	CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn	909
QY	1744	CATGCCATC 1752	
Db	910	HisAlaIle 912	

RESULT 3
 Q6ZMQ2
 ID Q6ZMQ2 PRELIMINARY; PRT; 796 AA.
 AC Q6ZMQ2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ16766.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```

Db      727 r1e1leLeuPheHisProGluGlnAsnValProLysArgLysArgSerLeuLysAlaVal 747
Qy      1605 GGTACCCCGCCGACCATGTCTCAACAACTTTCACAGAGGCGCACTTCAGGCCCAATGG 1664
Db      747 ValThrAlaAlaThrMetSerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGI 767
Qy      1665 GGAAGCCCAATCAGAGCTGTGTGAGAACTTGAGAGCCCGCCGCTGGCTACCAACAGAC 1724
Db      767 yGluAlaLysSerGluLeuCysGlyAsnLeuGluAlaProAlaLeuAlaThrLysGlnTh 787

Qy      1735 TCACTACCTACACCAACCATGCCATC 1752
Db      787 rTyrValThrTyrThrAsnHisAlaIle 796

RESULT 4
Q62916 PRELIMINARY; PRT; 983 AA.
AC Q62916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Metabotropic glutamate receptor 4b..
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Hara P.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U47331; AAA88788.1; -.
DR HSSP; P23385; LEWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mtglu_receptor.
DR InterPro; IPR001786; Mtglu_receptor4.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR01054; MTABOTROP4R.
DR PRINTS; PR00593; MTABOTROPICR.
DR PROSITE; PS00379; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
DR Receptor.
SQ SEQUENCE 983 AA; 109276 MW; 072F0D8B3A840A80 CRC64;

Alignment Scores:
Pred. No.: 6,26e-155 Length: 983
Score: 2732.00 Matches: 535
Percent Similarity: 85.09% Conservative: 7
Best Local Similarity: 83.99% Mismatches: 34
Query Match: 82.71% Indels: 61
DB: 2 Gaps: 7

US-10-828-332-6 (1-1755) x Q62916 (1-983)
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Db :::::
330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
Qy 64 AGCCGACGCTGACAAACAGCGCACATCTGGTTGCGAGTCTGGGAGGACAAAC 123
Db :::::
350 SerArgThrLeuAspAsnArgAsnIleThrPheAlaGluPheTrpGluAspAsn 369
Qy 124 TTCCATTGCAAGTTGAGCGGCACCGCTCAAGAGAGGGAAGCCACATCAAGAAGTGACCC 183
Db :::::

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Db      370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLeuLysCysThr 389
Qy      184 AACCGAGAGCGCATCGGCGCAGGACTCGGCGCTATCAGCAGAGGAGGGAAGGTCCAGTTCGTG 243
Db      390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGlnGlnGluGlyLysValGlnPheVal 409
Qy      244 ATTGACGCTGTGTACGCCATCGGCGCACGCGTGCACGCCCATGCACCGTGACCTGTGTCCC 303
Db      410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
Qy      304 GGCCGCTAGACTCTGCCCTCGCATGACCCCGTGGATGGCACCACCGAGTCTTAAGTAC 363
Db      430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
Qy      364 ATCAGGAACGTCAACTTCTCAGGCATTGCGGGGAACCTGTAACTTCAATGAGAACGGA 423
Db      450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGlnAsnGly 469
Qy      424 GACGCACCGGCGCTACGACATCTACAGTACCACCTGCGCAATGGCTCGGCCGAGTAC 483
Db      470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 489
Qy      484 AAGTCAATCGGCTCGTGGACAGACACCTGACACCTCAGATAGAGCGGATGCAGTGCCA 543
Db      490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 509
Qy      544 GGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCTGCCCTGCCACCGCGGGAGCGA 603
Db      510 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
Qy      604 AAGAAGACTGTGTGAAGGCGCTGCTGTGCTGGCACCTGCGAGCCCTGCACCGGTACCAG 663
Db      530 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 549
Qy      664 TACCAAGTGAGCCCTACACTGTAAAGACCTGCGCCCTACGACATCGCGCCCAACAGAAC 723
Db      550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
Qy      724 CGCAGAGCTGCCAGCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGCTGGCGCGTG 783
Db      570 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 589
Qy      784 CTGCCCCCTCTTCTGGCGCTGGTGGGCATCGCCGCCACGCTGTTCTGTTGGTGGTCCACGTTT 843
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Qy      844 GTGGCTTACAAAGATACCCCATCTGACAGCCCTCGGCGCGGGAACCTGAGTACGTGCTG 903
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Qy      904 CTGGCGGGCATCTTTCTGTGCTAGCCCACTACCTTCTCATGATCGCAGACCGGACCTG 963
Db      630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
Qy      964 GGGACCTGTTCTCGCTCCCGCATCTTCTAGGGCTCGGCATGAGCATCAGCTACGCGGCC 1023
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Qy      1024 CTGCTGACCAAGACCAACCGCATTTACGCATCTTTGAGAGGGCAACCGTTCGGTCACT 1083
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Qy      1084 GCCCGGGTTTCATCAGCCGGCTCGCAGCTGGCCCATCACCTTTCATCTCTCCCTG 1143
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Qy      1144 CAGTGTCTCGGCATCTCGTGTGCTGTTGGTGGACCCCTCCACCTCGGTGGTGGACTTC 1203
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Qy      1204 CAGACCAACAGCACTTGACCCCGCTTTCGCCAGGGCGGTGCTCAAGTGGCAGACTCTCG 1263
Db      730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749

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QY 1264 GACCTCTCCTCATCTGCTGCTGGCTACAGCATCTCTGATGTCAGTGTACTGTG 1323
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 QY 1324 TAGCGCATCAAGACCGGCGTCCGAGACCTTCAACGAGCGCCCAAGCCCTCGGCTTC 1383
 DB 770 TyrAlaIleuSerThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
 QY 1384 ACCATGTACACCACTGCATTGTCTGGCTGGCTTCATCCCATCTCTTTTGGCACCCTCA 1443
 DB 790 ThrMetTyrThrThrCysIleValTTPLeuAlaPheIleProIlePheGlyThrSer 809
 QY 1444 CAGTCAGCGCAGCAAGCTGTACATTCACAGAACACCACTGACGGTCTCTCGTGTAGTCGAGC 1503
 DB 810 GinSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 829
 QY 1504 GCTTCAGTCTCCCTGGGATGCTCTACATGCCCAAGTCTACATCATCTCTCTCCAC--- 1560
 DB 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuLeuPheHisIle 849
 QY 1561 ---CCGAGCAGAACGTCGCCCAAGCGCAGTCTCAAGACCGCTGTCACCGCGCC 1617
 DB 850 PhePro-PheCysSerTyrProSer-----ProAlaIleCysProAl 863
 QY 1618 ACATGTCCCAACAGT----- 1633
 DB 863 aProCysProSerSerLeuSerCysProIleProAlaIlePheSerSerValProPr 883
 QY 1634 ---TCACAC----- 1639
 DB 883 oArgSerHisPheLeuProAlaPheProLeuLeuGlyPheIleHisGlnLeuPheHis 903
 QY 1640 -----AGAGGGCAACTTCAGGCCCAATGGGGAAGCCAAATCA 1677
 DB 903 sValAlaLysGluLysLysGlyGlyGlySerProProThrLysLysProlysG 923
 QY 1678 G-----AGCTGTGTGAACTCGAGACCCAG----- 1705
 DB 923 nLysLeuIleLeuSerValPheArgSerAlaAlaSerTyrTyrProValCysProCy 943
 QY 1706 -CGTGGTCCCAACAGACCTACGTCACTACCAACCATGCCATCT 1753
 DB 943 sGlyLeuGlnProAlaArgProProTyrProSerAlaValCysProAla 959
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 ID Q68EF4 PRELIMINARY; PRT; 832 AA.
 AC Q68EF4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Mouse;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodargren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalilus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Mouse;
 RA Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC080284; AAH80284.1; -;
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR00162; Mtblu receptor.
 DR InterPro; IPR001786; Mtblu_receptor4.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PRINTS; PR01054; MTABOTROPICAR.
 DR PRINTS; PR00593; MTABOTROPICR.
 DR PROSITE; PS00379; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 832 AA; 92832 MW; 2B90570F77861FB1 CRC64;
 Alignment Scores:
 Pred. No.: 7,35e-144 Length: 832
 Score: 2546.50 Matches: 477
 Percent Similarity: 56.41% Conservative: 6
 Best Local Similarity: 95.21% Mismatches: 17
 Query Match: 77.10% Indels: 1
 DB: 2 Gaps: 1
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 QY 7 GGGGTATCATCATCTTTTCCCAACGAGATGACA---TCAGGGTTCCGACGATACCTTCTCC 63
 DB 330 GlyAlaValThrIleLeuProLysArgThrSerValArgGlyPheAspArgTyrPheSer 349
 QY 64 AGCCGACGTCGGACAAACAACAGCGCAACATCTGTTTCCGAGTCTCTGGGAGGACAC 123
 DB 350 SerArgThrLeuAspAsnAsnArgAsnIleTyrPheAlaGluPheTyrGluAspAsn 369
 QY 124 TTCCATTGCAAGTTGAGCGCCGCGCTCAAGAGGAAGCCACATCAAGAAGTGCCACC 183
 DB 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 389
 QY 184 AACCGAGAGCGCATCGGACGAGTCTCGCCCTATGAGCAGGAGGAGGAGGAGTGCAGTTCGTG 243
 DB 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
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 QY 364 ATCAGGAACGTCAACTCTTCAGGCATTCGCGGGAACCTGTAACTTCAATGAGAACGGA 423
 DB 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 CAGCAGCGGGCGCTACGACATCTACAGTACCACTGCGCACTGCGCACTGCGCCGACGATAC 483
 DB 470 AspAlaProGlyArgTyrAspIleTyrGlnArgArgAsnGlySerAlaGluTyr 489


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QY 484 AAGTCTATCGGCTGTCGACAGACACCTGTCACCTCAGAAATAGACGGATCGATGGCCA 543
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QY 784 CTGCCCCCTTCTGCGCGTGGTGGCATCGCGCCACGCTGTCTCGTGGTGGTCACTGTTT 843
Db 590 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValValThrPhe 609
QY 844 CTGCGCTACACGATACCCCATCGTCAAGCGCTCGCGCGGAGTGGAGTCACTGCTGCTG 903
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Db 830 Ala 830
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MGR8 HUMAN
ID MGR8_HUMAN STANDARD; PRT; 908 AA.
AC 000222; OL5493; O95945; O95946;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 8 precursor (mGluR8).
DE Name=GRM8; Synonyms=GPCR1H, MGLUR8;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=97446143; PubMed=9299241; DOI=10.1016/S0169-328X(97)00277-5;
Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
Rostek P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.;
"Group III human metabotropic glutamate receptors 4, 7 and 8:
molecular cloning, functional expression, and comparison of
pharmacological properties in RGT cells.";
Brain Res. Mol. Brain Res. 53:88-97(1998).
[2]
SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=97446143; PubMed=9299241; DOI=10.1016/S0169-328X(99)00050-9;
Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui L.-C.;
"The human metabotropic glutamate receptor 8 (GRM8) gene: a
disproportionately large gene located at 7q31.3-q32.1.";
Genomics 44:232-236(1997).
[3]
SEQUENCE FROM N.A. (ISOFORMS B AND C).
TISSUE=Petal brain.
MEDLINE=99234274; PubMed=10216218; DOI=10.1016/S0169-328X(99)00050-9;
Malherbe P., Kratzelstein C., Lundstrom K., Richards J.G., Faull R.L.M.,
Mutel V.;
"Cloning and functional expression of alternative spliced variants of
the human metabotropic glutamate receptor 8.";
Brain Res. Mol. Brain Res. 67:201-210(1999).
-1- FUNCTION: Receptor for glutamate. The activity of this receptor is
mediated by a G-protein that inhibits adenylyl cyclase activity.
-1- SUBUNIT: Interacts with PRKCAP (By similarity).
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=A; Synonyms=mGluR8a;
IsoId=000222-1; Sequence=Displayed;
Name=B; Synonyms=mGluR8b;
IsoId=000222-2; Sequence=VSP_002032;
Name=C; Synonyms=mGluR8c;
IsoId=000222-3; Sequence=VSP_002033, VSP_002034;
-1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
-----
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or send an email to license@isb-sib.ch).
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EMBL; U92459; AAB51764.1; --
EMBL; U95025; AAB72040.1; --
EMBL; AJ236921; CAB36968.1; --
EMBL; AJ236922; CAB36969.1; --
HSSP; P23385; 1EMT.
Gene; HGNC:4600; GRM8.
MIM; 601116; --
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0008087; P:metabotropic glutamate, GABA-B-like recepto. . .; TAS.
GO; GO:0007194; P:negative regulation of adenylyl cyclase ac. . .; TAS.
GO; GO:0007601; P:visual perception; TAS.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000337; GPCR_Mgr.
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DR	InterPro: IPR000162; Mtblu_receptor.	Db	347	SerArgThrLeuAlaAsnAsnArgAsnValTrpPheAlaGluPheTrpGluGluAsn	366
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DR	Pfam: PF01093; 7tm3; 1.	Db	367	PheGlyCysLeuLeuGlySerHisGly--LysArgAsnSerHisGlyLeuLeuGlySerHis	385
DR	PRINTS: PR00248; GPCRMR.	Qy	184	AACGAGAGCGATCGGCGAGACTCGCGCTATGAGCAGGAGGAGGAGGAGTGCAGTTCGTG	243
DR	PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.	Db	386	GlyLeuGluArgIleAlaArgAspSerSerTyrGluGlnGluGlyLysValGlnPheVal	405
DR	PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.	Qy	244	ATTGACGCTGTGTAGCGATCGGCGACCGCTGCACGCGCTGCACCGTGCACCTGTGTCC	303
DR	PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.	Db	406	IleAspAlaValTyrSerMetAlaTyrAlaLeuHisAsnMetHisLeuAspLeuGlySer	425
DR	PROSITE: PS00982; G_PROTEIN_RECP_F3_4; 1.	Qy	304	GGCGCGTAGGACTTCGCCCTCGCATGACCGCGCGTGGATGGCACCACCGCTGTAAAGTAC	363
KW	Alternative splicing; G-protein coupled receptor; Glycoprotein;	Db	426	GlyTyrIleGlyLeuGlyProArgMetSerThrIleAspGlyLysGluLeuGlyTyr	445
KW	Multigene family; Olfaction; Polymorphism; Signal; Transmembrane.	Qy	364	ATCAGGAACGTCAACTTCTCAGGCAATTCGGGGGAACTGTAACTTCAATGAGAACGGA	423
FT	SIGNAL 1 33	Db	446	IleArgAlaValAsnPheAsnGlySerAlaGlyThrProValThrPheAsnGluAsnGly	465
FT	CHAIN 34 908	Qy	424	GACGACCGGCGCTACGACATCTACCAGTACCACTGCGCAATGGCTCGSCCGAGTAC	483
FT	DOMAIN 34 583	Db	466	AspAlaProGlyArgTyrAspIlePheGlnIleThrAsnLysSerThrGluTyr	485
FT	TRANSMEM 584 608	Qy	484	AAGTCATCGGCTCGTGACAGACACCGCTGCACCTCAGAAATAGAGCGGATGAGTGGCCA	543
FT	DOMAIN 609 620	Db	486	LysValIleGlyHisTrpThrAsnGlnLeuHisLeuValGluAspMetGlnTrpAla	505
FT	TRANSMEM 621 641	Qy	544	GGGAGTGGCCAGAGCTCCCGGCTCATCTGCGAGTCTGCCCTGCGACCGCGGGAGCGA	603
FT	DOMAIN 642 647	Db	506	HisArgGluHisThrHisProAlaSerValCysSerLeuProCysLeuProGlyGluArg	525
FT	TRANSMEM 648 668	Qy	604	AAGAGACTGTGAAGGCGATGCTTGTCTGCTGGCACTCGGAGCCCTCGACCGGTACCCAG	663
FT	DOMAIN 669 695	Db	526	LysLysThrValValGlyValProCysSerTrpHisCysGluArgCysGluGlyTyrAsn	545
FT	TRANSMEM 696 716	Qy	664	TACCAAGTGGAGCCGCTACACCTGTAAGACCTGCCCCCTACGACATGCGCGCCACAGAGAAC	723
FT	DOMAIN 717 746	Db	546	TyrGlnValAspGluLeuSerCysGluLeuCysProLeuAspGlnArgProAsnMetAsn	565
FT	TRANSMEM 747 768	Qy	724	CGCAGAGCTCCAGCCCATCCCATCTCAAGTTGGAGTGGGACTCCCGTGGGCGGTG	783
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FT	TRANSMEM 782 803	Qy	784	CTGCCCTCTTCTGGCGGTGGTGGCATCCCGCCAGCTGCTGCTGCTGCTGCTGCTGCTT	843
FT	DOMAIN 804 818	Db	586	ValProValPheValAlaIleLeuGlyIleIleAlaThrPheValIleValThrPhe	605
FT	TRANSMEM 819 843	Qy	844	GTGCGCTACAAACGATACCCCATCGTCAAGGCTCGGCGCGGAACTGAGCTACGTGCTG	903
FT	DOMAIN 844 908	Db	606	ValArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrValLeu	625
FT	CARBOHYD 95 95	Qy	904	CTGCGGGGCACTTCTTGTGCTAGCCCACTACCTTCTCATGATCGCAGAGCGCGACCTG	963
FT	CARBOHYD 298 298	Db	626	LeuThrGlyIlePheLeuCysTyrSerIleThrPheLeuMetIleAlaAlaProAspThr	645
FT	CARBOHYD 452 452	Qy	964	GGGACCTGTTCTCGCCGCGCATCTTCTAGGCTCGGCGCATGAGCTACGCTACCGGCC	1023
FT	CARBOHYD 480 480	Db	646	IleIleCysSerPheArgValPheLeuGlyLeuGlyMetCysPheSerTyrAlaAla	665
FT	CARBOHYD 565 565	Qy	1024	CTGCTGACCAAGACCAACCGCATTTACCGCATCTTTAGAGCGGGCAACCGTTCAGT	1083
FT	VARSPLIC 893 908	Db	666	LeuLeuThrLysThrAsnArgIleHisArgIlePheGluGlnGlyLysSerValThr	685
FT		Qy	1084	GCCCGCGTTCATCAGCCCGCTCGCAGCTGGCCATCCTTCATCTCATCTCTCCCTG	1143
FT		Db	686	AlaProLysPheIleSerProAlaSerGlnLeuValIleThrPheSerLeuIleSerVal	705
FT		Qy	1144	CAGTGTCTCGGCATCTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1203
FT		Db	706	GlnLeuLeuGlyValPheValTrpPheValValAspProProHisIleIleIleAspTyr	725

Alignment Scores:

Pred. No.:	9,938-134	Length:	908
Score:	2377.00	Matches:	438
Percent Similarity:	85.08%	Conservative:	58
Best Local Similarity:	75.13%	Mismatches:	85
Query Match:	71.96%	Indels:	2
DB:	1	Gaps:	2

US-10-828-332-6 (1-1755) x MGR8_HUMAN (1-908)

Qy	7	GGGCTATCATCATCTTTGCAAGGAGGATGACA---TCAGGTTGCGACCGATCTTCTCC	63
Db	327	GlyAlaValThrIleLeuProLysArgAlaSerIleAspGlyPheAspArgTyrPheArg	346
Qy	64	AGCCGACGCTGGACAACAAGGCGCAACATCTCGTGTGCGGATCTCTGGGAGGACAAC	123

Qy	1204	CAGGACCAACGGGACACCTTGACCCCGCGCTTTGCCAGGGCGGTGCTCAAGTGCACATCTCG	1263
Db	726	GlyGluGlnArgThrLeuAapProGluLysAlaArgGlyValLeuLysCysAepIleSer	745
Qy	1264	GACCTGTCCCTCATCTGCTGCTGGGTACAGCATGCTGCTGATGTCACGTGTACTGTG	1323
Db	746	AspLeuSerLeuIleCysSerLeuGlyTy-SerIleLeuLeuMetValThrCysThrVal	765
Qy	1324	TAGCCCATCAAGACCCGAGCGGTGCCGAGACCTTCAACGAGGCCAAGCCATCGGCTTC	1383
Db	766	TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe	785
Qy	1384	ACCATGTACACCACTGTCATTGTCTGGCTGGCTTCATCCCATCTTTTGGCACCTCA	1443
Db	786	ThrMetTyThrThrCysIleIleTrpLeuAlaPheIleProIlePheGlyThrAla	805
Qy	1444	CAGTCAGCCGCAAGCTGTATCATCCAGACAACACATGACGGTCTCCGTGAGTCTGAGC	1503
Db	806	GlnSerAlaGluLysMetTyIleGlnThrThrThrLeuThrValSerMetSerLeuSer	825
Qy	1504	GCTTCAGTGTCCCTGGGATGCTTACATGCCCAAGTCTACATCATCTCTCTTCCACCCG	1563
Db	826	AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrlleIleIlePheHisPro	845
Qy	1564	GAGCAGAAAGTGGCCCAAGCGCAAGCGAGTCTCAAAGCGGTGGTCTACCGCGCCACCATG	1623
Db	846	GluGlnAsnValGlnLysArgLysArgSerPheLysAlaValValThrAlaAlaThrMet	865
Qy	1624	TCCAAACAGTTTCACACAGAAGGGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG	1683
Db	866	GlnSerLysLeuIleGlnLysGlyAsnAspArgProAsnGlyGluValLysSerGluLeu	885
Qy	1684	TGTGAGAACCTGGAGACCCGCGCTGGCTACCAACAGACCTACGTCACCTACACCAAC	1743
Db	886	CysGluSerLeuGluThrAsnThrSerSerThrLysThrThrTyrlleSerTySerAsn	905
Qy	1744	CATGCCATC 1752	
Db	906	HisSerIle 908	
RESULT 7			
Q6B964		PRELIMINARY;	
ID	Q6B964	PRT;	908 AA.
AC	Q6B964;		
DT	25-OCT-2004 (TrEMBLrel. 28, Created)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Metabotropic glutamate receptor 8A.		
GN	Name=Gm8A;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI	TaxID=10090;		
RP	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/c; TISSUE=Whole brain;		
RA	Guo J., Ikeda S.R.;		
RT	"Cloning of the mouse metabotropic glutamate receptor 8A.";		
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY673682; AAU76980.1; -		
DR	GO; GO:0016021; C:integral to membrane; TAS.		
DR	GO; GO:0001642; F:group III metabotropic glutamate receptor a. . .; IDA.		
DR	InterPro; IPR001828; ANF_receptor.		
DR	InterPro; IPR000337; GPCR_Mgr.		
DR	InterPro; IPR000162; Mrglu_receptor.		
DR	InterPro; IPR000144; Mrglu_receptor8.		
DR	InterPro; IPR011500; NCD3G_GPCR.		
DR	Pfam; PF00003; 7cm_3; 1.		
DR	Pfam; PF01094; ANF_receptor; 1.		
DR	Pfam; PF07562; NCD3G; 1.		
DR	PRINTS; PR00248; GPCRMRG.		
DR	PRINTS; PR01058; MTABOTROPIC8R.		

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QY      844 GTGGCGTACACGATACCCCATCGTCAAGGCGCTGGGCGCGGAACCTGAGCTACGTGCTG 903
Db      606 ValArgTyAsnAspThrProileValArgAlaSerGlyArgGluLeuSerTyValLeu 625
QY      904 CTGGGGGGCATCTTTCTGTGTACGGCACTACCTTCTCATCATCGACGGCGGACCTG 963
Db      626 LeuThrGlyLeuPheLeuGlySerIleThrPheLeuMetIleAlaAlaProAspThr 645
QY      964 GGGACCTGTTCTCGCGCGCATCTTCTAGGCGCTGGCATGAGCATCACTACGGCGC 1023
Db      646 IleIleCysSerPheArgGlyLeuGlyLeuGlyMetCysPheSerTyAlaAla 665
QY      1024 CTGTGTACCAAGACCAACCGCATTTACCGCATCTTTGACGAGGGCAAAAGCGTGGTCA 1083
Db      666 LeuLeuThrLysThrAsnArgIleHisArgIlePheGluGlnGlyLysSerValThr 685
QY      1084 GCCCGCGTTTCATCAGCGCGCGCTCGAGCTGGCCATCACCTTCATCTCATCTCCCTG 1143
Db      686 AlaProLysPheIleSerProAlaSerGlnLeuValIleThrPheSerLeuIleSerVal 705
QY      1144 CAGCTGCTCGCATCTGCGTGTGTGTGGTGGACCCCTCCCATCTCGGTGGTCACTTC 1203
Db      706 GlnLeuLeuGlyValPheValTrpPheValAlaAspProHisThrIleIleAspTyr 725
QY      1204 CAGGACCAACGACACTTGACCCCGCTTTGCGAGGGCGTCTCAAGTGGACATCTCG 1263
Db      726 GlyGluGlnArgThrLeuAspProGluAenAlaArgGlyValLeuLysCysAspIleSer 745
QY      1264 GACCTGCTCCCTCATCTGCTGTGGCTACACATGCTGCTCATGTGTCACTGTTACTGTG 1323
Db      746 AspLeuSerLeuIleCysSerLeuGlyTySerIleLeuLeuMetValThrCysThrVal 765
QY      1324 TACGCCATCAAGACCGAGCGCTGCCGAGACTTCAACGAGCGCAAGCCCATCGCTTC 1383
Db      766 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 785
QY      1384 ACCATGTACACCACTGCACTGTCTGTGGTGGCTTCATCCCATCTTTTGGCACCTCA 1443
Db      786 ThrMetTyThrThrCysIleIleTrpLeuAlaPheIleProIlePheGlyThrAla 805
QY      1444 CAGTCAGCGCAGCAAGCTGATCAGACCAACCACTGACCGTCTCGTGAAGTCTGAC 1503
Db      806 GlnSerAlaGluLysMetTyIleGlnThrThrThrLeuThrValSerMetSerLeuSer 825
QY      1504 GCTTCAGTGTCTCGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCACCG 1563
Db      826 AlaSerValSerLeuGlyMetLeuTyMetProLysValTyIleIleIlePheHisPro 845
QY      1564 GAGCAGACGTCGCCAAGCGCAGCTCTCAAAGCGGTGGTCAACCGCCCGCCACCATG 1623
Db      846 GluGlnAenValGlnLysArgLysArgSerPheLysAlaValThrAlaAlaThrMet 865
QY      1624 TCCACACAGTTACACAGAGGGCACTTCAGGCCCATGGGAGGCCAATCAGAGCTG 1683
Db      866 GlnSerLysLeuIleGlnLysGlyAsnAspArgProAsnGlyGluValLysSerGluLeu 885
QY      1684 TGTGAGACCTGGAGACCCGCGCTGCTACCAACAGACCTAGCTACCTACACCAAC 1743
Db      886 CysGluSerLeuGluThrAsnThrSerSerThrLysThrThrTyIleSerTySerAsn 905
QY      1744 CATGCCATC 1752
Db      906 HisSerIle 908

RESULT 8
MGR8 RAT
ID MGR8 RAT          STANDARD;          PRT;          908 AA.
AC P70579;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 8 precursor (mGluR8).

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GN      Name=Grm8; Synonyms=Gprc1h, Mglur8;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97168760; PubMed=9016353;
RA      Saugstad J.A., Kinzie J.M., Shinohara M.M., Segerson T.P.,
RT      Westbrook G.L.;
RT      "Cloning and expression of rat metabotropic glutamate receptor 8
RL      reveals a distinct pharmacological profile.";
Mol. Pharmacol. 51:119-125(1997).
RN      [2]
RP      INTERACTION WITH PKCABP.
RX      MEDLINE=20571397; PubMed=11122333;
RA      El Far O., Airas J., Wischmeyer E., Nehring R.B., Karschin A.,
RT      Betz H.;
RT      "Interaction of the C-terminal tail region of the metabotropic
RT      glutamate receptor 7 with the protein kinase C substrate PICK1.";
Eur. J. Neurosci. 12:4215-4221(2000).
CC      - FUNCTION: Receptor for glutamate. The activity of this receptor is
CC      mediated by a G-protein that inhibits adenylate cyclase activity.
CC      - SUBUNIT: Interacts with PKCABP.
CC      - SUBCELLULAR LOCATION: Integral membrane protein.
CC      - TISSUE SPECIFICITY: Prominent expression in olfactory bulb,
CC      pontine gray, lateral reticular nucleus of the thalamus, and
CC      piriform cortex. Less abundant expression in cerebral cortex,
CC      hippocampus, cerebellum, and mammillary body.
CC      - SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      HMBL; U63288; AAB09537.1; -.
CC      HSSP; P23385; 1EWT.
DR      RGD; 619858; Grm8.
DR      InterPro; IPR001828; ANF receptor.
DR      InterPro; IPR000337; GPCR_Mgr.
DR      InterPro; IPR000162; Mglu receptor.
DR      InterPro; IPR000144; Mglu_receptor8.
DR      Pfam; PF00003; 7tm_3; 1.
DR      Pfam; PF01094; ANF_receptor; 1.
DR      PRINTS; PR00248; GPCRMR.
DR      PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR      PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR      PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR      PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
KW      G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW      Signal; Transmembrane.
FT      SIGNAL          1..33
FT      CHAIN           34..908
FT      DOMAIN          34..583
FT      DOMAIN          584..608
FT      TRANSMEM        609..620
FT      DOMAIN          621..641
FT      TRANSMEM        642..647
FT      DOMAIN          648..668
FT      TRANSMEM        669..695
FT      DOMAIN          696..716
FT      TRANSMEM        717..746
FT      DOMAIN          747..768
FT      TRANSMEM        769..781
FT      DOMAIN          782..803
FT      TRANSMEM        804..818
FT      DOMAIN          819..843
FT      TRANSMEM        844..908
FT      DOMAIN          909
FT      CARBOHYD        95

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FT CARBOHYD 298 298 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 452 452 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 480 480 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 565 565 N-linked (GlcNAc...) (Potential)
SQ SEQUENCE 908 AA; 101866 MW; FCAB54CB8E3DD915 CRC64;

Alignment Scores:

Pred. No.: 2,27e-133 Length: 908
Score: 2371.00 Matches: 436
Percent Similarity: 85.08% Conservative: 60
Best Local Similarity: 74.79% Mismatches: 85
Query Match: 71.78% Indels: 2
DB: 1 Gaps: 2

US-10-828-332-6 (1-1755) x MGR8_RAT (1-908)

QY 7 GGGGTATCATCTTTGCCAACGAGGATGACA---TCAGGGTTCGACCGCATCTTCC 63
DB GlyAlaValThrIleLeuProLysArgAlaSerIleAsePheAspArgTyrPheArg 346
QY 64 AGCCGACGCTGGACAAACAGCGCAACATCTGTTGCGAGTTCGGGAGGACAAAC 123
DB SerArgThrLeuAlaAsnAsnArgAsnValTrpPheAlaGluPheTrpGluGluAsn 366
QY 124 TTCCATTGCAAGTTGAGCGCGCTCAGAGGAGGAGCAACATCAAGAAAGTGCAAC 183
DB PheGlyCysLysLeuGlySerHisGly---LysArgAsnSerHisIleLysCysThr 385
QY 184 AACCGAGAGCCATCGGCGAGCATCGCCCTATGACGAGGAGGAGGAGTTCAGTTG 243
DB GlyLeuGluArgIleAlaAspSerSerTyrGluGlnGluGlyLysValGlnPheVal 405
QY 244 ATTGACGCTGTAGCCATGGCCACCGCTGACCGCCATGACCGTGCCTGTGCCCC 303
DB IleAspAlaValTyrSerMetAlaTyrAlaLeuHisAsnMetHisLysGluArgCysPro 425
QY 304 GGCCGCTAGACTCTGCGCTCGATGGACCGCCGCGGATGGCACCGTCTTAAGTAC 363
DB GlyTyrIleGlyLeuCysProArgMetValThrIleAspGlyLysGluLeuGlyTyr 445
QY 364 ATCAGGACGTCATCTTCAGGCATTCGGGGAAACCCCTGTAACCTTCAATGAGACGA 423
DB IleArgAlaValAsnPheAsnGlySerAlaGlyThrProValThrPheAsnGluAsnGly 465
QY 424 GACCCACCGGCGCTACGATCTACAGTACCACTGCCCAATGGCTCGCGCGAGTAC 483
DB AspAlaProGlyArgTyrAspIlePheGlnTyrGlnIleAsnAsnLysSerThrGluTyr 485
QY 484 AAGGTCTACGCTCGTGACAGACACCTGCACCTCAGAAATAGAGCGGATGCAGTGGCCA 543
DB LysIleIleGlyHisTrpThrAsnGlnLeuHisLeuLysValGluAspMetGlnTrpAla 505
QY 544 GGGAGTGGCCAGCAGTCCCGCTCCATCTGCACTGCGCTCCAGCCCGGGAGCGA 603
DB AsnArgGluHisThrHisProAlaSerValCysSerLeuProCysLysProGlyGluArg 525
QY 604 AAGAACTGTAGGGCATCGCTGCTGCGCACTCGGACCTCGACCGGTACCAG 663
DB LysLysThrValLysGlyValProCysCysTrpHisCysGluArgCysGluGlyTyrAsn 545
QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATGCGCGCCACAGAGAAC 723
DB TyrGlnValAspGluLeuSerCysGluLeuCysProLeuAspGlnArgProAsnIleAsn 565
QY 724 GCGCAGAGCTCCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCCTGGCGCGTG 783
DB ArgThrGlyCysGlnArgIleProIleIleLysLeuGluTrpHisSerProTrpAlaVal 585
QY 784 CTGCCCCCTCTTCCTGGCGCTGGTGGCATCCCGCCAGCTGTTCTGGTGGTTCACGTTT 843
DB ValProValPheIleAlaIleLeuGlyIleAlaIleThrPheValIleValThrPhe 605
QY 844 GTGCGCTACACGATACCCCATCTGTCAGAGCCTCGCGCGCGGAACTGAGCTAGTGTG 903

DB ValArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrValLeu 625
QY CTGGCGGGCATCTTCTGCTAGCCACTACCTTCTCTCATCTGATCGAGAGCCGAGCCTG 963
DB LeuThrGlyIlePheLeuCysTyrSerIleThrPheLeuMetIleAlaAlaProAspThr 645
QY 964 GGGACCTGTTGCTCCGCGCCGCTCTCTAGGGCTCGGCATGAGCATCAGCTACGCGGCC 1023
DB IleIleCysSerPheArgArgIlePheLeuGlyLeuGlyMetCysPheSerTyrAlaAla 665
QY 1024 CTGCTGACCAAGCAACACCATTTACCGCATCTTTCAGAGGAGGCAACCGTTCGTCAGT 1083
DB LeuLeuThrLysThrAsnArgIleHisArgIlePheGluGlnGlyLysLysSerValThr 685
QY 1084 GCGCGGCTTTCATCAGCCCGCGCTCGCAGTGGCCATCCTCATCTCTCATCTCCCTG 1143
DB AlaProLysPheIleSerProAlaSerGlnLeuValIleThrPheSerLeuIleSerVal 705
QY 1144 CAGCTGCTCGGCATCTCGGTGTGCTGCTGGTGACCCCTCCCACTCGGTGGACTTC 1203
DB GlnLeuLeuGlyValPheValTrpPheValValAspProHisThrIleIleAspTyr 725
QY 1204 CAGGACCAACGACATTTGACCCCGCTTTGCCAGGGCGTCTCAAGTGGGACATCTCG 1263
DB GlyGluGlnArgThrLeuAspProGluAsnAlaArgGlyValLeuLysCysAspIleSer 745
QY 1264 GACCTGCTCCCTCATCTGCTGCTGGCTACGACATGCTGCTGATGGTTCAGTGTACTGTG 1323
DB AspLeuSerLeuIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThrVal 765
QY 1324 TAGCCCATCAAGACCCGAGCGCTGCCGAGACCTTCAACAGAGGCAAGCCCATCGGTTC 1383
DB TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 785
QY 1384 ACCATGTACACCATCTGCTGCTGGCTGCTCATCCCATCTCTTTTGGCACCTCA 1443
DB ThrMetTyrThrThrCysIleIleTrpLeuAlaPheIleProIlePheGlyThrAla 805
QY 1444 CAGTCAGCCGACAGCTGTATCATCCAGACACCACTGAGCGTCTCGGTGAGTCTCAGC 1503
DB GlnSerAlaGluLysMetTyrIleGlnThrThrThrLeuThrValSerMetSerLeuSer 825
QY 1504 GCTTCACTGCTCCCTGGGATGCTCTACATGCCAAAGCTACATCATCTCTTCCACCCG 1563
DB AlaservAlserLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHisPro 845
QY 1564 GAGCAGAACCTGTGCCAAGCGCAGCGCTCTCAAGCGGTGTCACCGCGCCACCATG 1623
DB GluGlnAsnValGlnLysArgLysArgSerPheLysAlaValValThrAlaAlaThrMet 865
QY 1624 TCCAACAGTTTCACAGAGGCGCACTTCAGGCCCAATGGGAGGCCAATCAGAGCTG 1683
DB GlnSerLysLeuIleGlnLysGlyAsnAspArgProAsnGlyGluValLysSerGluLeu 885
QY 1684 TGTGAGAACTGGAGACCCCGCGCTGGCTACCAAAACAGACCTACGTACCTACCAACAC 1743
DB CysGluSerLeuGluThrAsnThrSerSerThrLysThrThrIleSerTyrSerAsn 905
QY 1744 CATGCCATC 1752
DB HisSerIle 908
RESULT 9
MGR8_MOUSE STANDARD; PRT; 908 AA.
AC P47743;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 8 precursor (mGluR8).
GN Name=Grm8; Synonyms=Gprclh, mGluR8;
OS Mus musculus (Mouse).

FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 486 486 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 572 572 N-linked (GlcNAc...) (Potential).
 FT VARIANT 433 433 Y -> F (in dbSNP:2234977).
 FT /FTID=VAR 003584.
 SQ SEQUENCE 915 AA; 102250 MW; CFF94E06B7F4919 CRC64;

Alignment Scores:

Pred. No.: 2,72e-124 Length: 915
 Score: 2219.00 Matches: 408
 Percent Similarity: 82.53% Conservative: 74
 Best Local Similarity: 69.86% Mismatches: 100
 Query Match: 67.18% Indels: 2
 DB: 1 Gaps: 2

US-10-828-332-6 (1-1755) x MGR7_HUMAN (1-915)

QY 7 GGGGTATCATCATCTTTGGCCACGAGGATGACA---TCAGGGTTCCACCGACTTCTCC 63
 DB 332 GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaTyrPheThr 351
 QY 64 AGCCGACCTGTCGACAAACAGCGCAACATCTGGTTTGGCCGAGTTCTGGGAGGACAAC 123
 DB 352 SerArgThrLeuGluAsnAsnArgArgAsnValTrpPheAlaGluTyrTrpGluGluAsn 371
 QY 124 TTCATTCGAAGTTGAGCCGCCCGCTCAAGAGGGAGCCACATCAAGAAGTGACCC 183
 DB 372 PheAsnCysLysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr 391
 QY 184 ACCGAGAGCGCATCGGAGGACTCGGCTATGACGAGGAGGGAGGTGCAAGTTCGTG 243
 DB 392 GlyGlnGluArgIleGlyLysAspSerAsnTyrGluGlnGluGlyValGlnPheVal 411
 QY 244 ATTGACGCTGTACGCCATGGCCACGCGCTGCACGCCCATCACCGTCACTGTGTC 303
 DB 412 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAsnLysAspLysCysAla 431
 QY 304 GGCCGGGTAGGACTCTGCCTCGCATGGAGCCCGCTGGATGGACCCAGCTGTCTTAAGTAC 363
 DB 432 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyLysLysLysLeuLeuLysTyr 451
 QY 364 ATCAGGAAGTCNACTTCAGGCATTGGGGGAACCTGTAACTTCAATGAGAACGGA 423
 DB 452 IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 471
 QY 424 GAGCACCGGGCGCTACCATCTACCACTGACCACTGCGCAATGCGCTCG---GCCGAG 480
 DB 472 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrThrAsnThrSerAsnProGly 491
 QY 481 TACAAGGTCACTGGCTCTGGGACAGACCACTGCACCTCAGATAGACGGATGCAGTGG 540
 DB 492 TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 511
 QY 541 CGAGGAGTGGCCAGCAGTGGCGCTCATCTGCACTGTGCTGCTGCCTGCAGCCGCGGAG 600
 DB 512 GlyLysGlyValArgGluIleProAlaSerValCysThrLeuProCysLysProGlyGln 531
 QY 601 CGAAGAAGACTGTGAAGGGCATGGCTTCTGCTGCACTGGAGCCCTGCACCGGTTAC 660
 DB 532 ArgLysLysThrGlnLysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr 551
 QY 661 CAGTACCAAGTGGCCGCTACACCTGTAAGACTGCGCCCTAGACATAGCGGCCACAGAG 720
 DB 552 GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu 571
 QY 721 AACCGCAGCAGTGGCCAGCCCATCCCATCGTCAAGTTGAGTGGAGTGGCGGTG 780
 DB 572 AsnArgThrGlyCysGlnAspIleProIleIleLysLeuGluTrpHisSerProTrpAla 591
 QY 781 GTGTGCTCCCTTCTCTGCGCGTGGTGGCATCGCGCCACCGCTGTTCGTGTGTCAGC 840
 DB 592 ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr 611

QY 841 TTTGTGCGGTACAAACGATACCCCATCGTCAAGGCTCGGGCGGGAACTGAGCTACGTG 900
 DB 612 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 631
 QY 901 GTGCTGGCGGGCATCTTTCTGTGTGTACGCCACTACTCTCTCATCTGATCCAGACGGGAC 960
 DB 632 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 651
 QY 961 CTGGGGACCTGTTCCTCGCCGATCTTCTAGGCGCTGGCATGAGCATCAGTACGGC 1020
 DB 652 ValAlaValCysSerPheArgArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla 671
 QY 1021 GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGGGCAAGCGTGGTC 1080
 DB 672 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysSerVal 691
 QY 1081 AGTGCCCGCGTTTCATCAGCCCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCC 1140
 DB 692 ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer 711
 QY 1141 CTGCACTGCTCGGCATCTGCGTGTGTGTGGTGGACCCCTCCCATCTCGGTGGTGGAC 1200
 DB 712 ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProProAsnIleIleIleAsp 731
 QY 1201 TTCAGGACCAACGAGACACTTGACCCCGCTTTGGCAGGGCGTGTCTCAAGTGGCATCTC 1260
 DB 732 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 751
 QY 1261 TCGGACCTGTCCTCATCTGCTGCTGGGTACAGCATGCTGCTGATGCTACGTTGCTACT 1320
 DB 752 ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr 771
 QY 1321 GTGTACGGCATCAAGACCCGAGCGCTGCCAGAGCTTCAACGAGGCGCAAGCCCATCGGC 1380
 DB 772 ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly 791
 QY 1381 TTCACCATGTACACCACTGCACTCTGGCTGGCTTCATCCCATCTTTTGGCACC 1440
 DB 792 PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThr 811
 QY 1441 TCACAGTCAGCGCAGCAAGCTGTATCTCAGACCAACACCACTGACCGTCTCCGTGAGTCTG 1500
 DB 812 AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrLeuThrIleSerMetAsnLeu 831
 QY 1501 AGCGTTCAGTGTCTCGGGATGCTTACATGCTCCCAAGTCTACATCATCTCTTCCAC 1560
 DB 832 SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHis 851
 QY 1561 CGGAGCAGACGTCGCCAAGCGCAGCTCTCAAAGCGGTGTCAACCGCGCCACC 1620
 DB 852 ProGluLeuAsnValGlnLysArgLysArgSerPheLysAlaValThrAlaAlaThr 871
 QY 1621 ATGTCCACAAGTTCACACAGAGGGCAACTTCAGGCCCAATGGGGAGGCAAAATCAGAG 1680
 DB 872 MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu 891
 QY 1681 CTGTGTGAGAACCTGGAGACCCCGCTGTACCAACACACACCTAGCTACCTACCTACAC 1740
 DB 892 LeuCysGluAsnValAspProAsnSerProAlaAlaLysLysLysTyrValSerTyrAsn 911
 QY 1741 AACCATGCCATC 1752
 DB 912 AsnLeuValIle 915

RESULT 11

Q68ED2 PRELIMINARY; PRT; 915 AA.
 ID Q68ED2
 AC Q68ED2; (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE Grm7 protein.

GN Name=Gxm7;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner S., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshilyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettenan M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RC Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080315; AAH80315.1; -;
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mtblu_receptor.
DR InterPro; IPR001883; Mtblu_receptor7.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR01057; MTABOTROPCTR.
DR PRINTS; PR00593; MTABOTROPCTR.
DR PROSITE; PS00379; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 915 AA; 102218 MW; F0AF7AEDBFBCF71 CRC64;
Alignment Scores:
Pred. No.: 5,42e-124 Length: 915
Score: 2214.00 Matches: 407
Percent Similarity: 82.53% Conservative: 75
Best Local Similarity: 69.68% Mismatches: 100
Query Match: 67.03% Indels: 2
DB: 2 Gaps: 2
US-10-828-332-6 (1-1755) x Q68ED2 (1-915)
QY 7 GGGGTATCATCATCTTTGCCACGAGGATGACA---TCAGGGTTCGACCGGATCTTC 63
DB 332 GlyAlaIleThrIleGlnProlysAlaThrValGluGlyPheAspAlaIleThrPheThr 351
QY 64 AGCCGCGAGCTGGACAAACAGCGCCCAACACTCTCGTTTGGCGAGTTCTGGGAGACAAAC 123
DB 352 SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTrpTrpGluAsn 371
QY 124 TTCATTGCAAGTTGAGCGGCCACCGCTCAAGAGGGGAAGCCACATCAAGAGTGCACC 183
DB 372 PheAsnCysLysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr 391

184 AACCGAGAGCGCATCGGGCAGGACTCGGCCTATGAGCAGGAGGGAAGGTGCAGTTCTGTG 243
DB 392 GlyGlnGluArgIleGlyLysAspSerAsnTyrGluGlnGlyLysValGlnPheVal 411
QY 244 ATTGACGCTGTGTACGCGTGGCGCACGCGCTGCACGCCATGCACCGCTGCTGTGTC 303
DB 412 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAsnLysAspLeuLysCysAla 431
QY 304 GGCGCGTAGGACTCTCGCCTCGCATGAGACCCCGTGGATGGCACCACCGCTTAAGTAC 363
DB 432 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyGlyLysLysLeuLeuLysTyr 451
QY 364 ATCAGGAACGTCAACTCTCAGGATTGCGGGGAACCCCTGTAACTTCAATTCAGAACCGGA 423
DB 452 IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 471
QY 424 GAGCACCGGGCGCTACGACATCTACAGTACCAACTGCGCAAT---GGTCCGGCGGAG 480
DB 472 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrThrAsnThrThrAsnProGly 491
QY 481 TACAGGTATCGCTCGTGGACAGACACCTGCACCTCAGAAATAGACCGGATGCAGTGG 540
DB 492 TyrArgLeuIleGlyGlnTyrThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 511
QY 541 CCAGGAGTGGCCACGACGCTGCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCCGGGAG 600
DB 512 GlyLysGlyValArgGluIleProProSerValCysThrLeuProCysLysProGlyGln 531
QY 601 CGAAGAAAGACTGTGAAGGGCATGGCTTGTCTGTCGACCTGCGAGCCCTGACCGGTAC 660
DB 532 ArgLysLysThrGlnLysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr 551
QY 661 CAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATCGCGCCACAGAG 720
DB 552 GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu 571
QY 721 AACCGCACGAGCTGCCAGCCCATCCCATCGTCAAGTTGGATGGGACTCGCCCTGGGCC 780
DB 572 AsnArgThrGlyCysGlnAsnIleProIleLysLeuGluTrpHisSerProTyrAla 591
QY 781 GTGTGCGCTCTTCCTGCGCGGTGGGATGCCCGCCAGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 592 ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr 611
QY 841 TTTGTGCGCTACACGATACCCCATCGTCAAGSCCTCGCGCGGGAACCTGAGCTACGTG 900
DB 612 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 631
QY 901 CTGCTGCGGGCATCTTTCTGTGCTAGCCCACTACCTTCCTCATGATCGCAGACCCGAC 960
DB 632 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 651
QY 961 CTGGGAGACTGTCCTCCCGCCATCTTCTAGGGTTCGGCATGAGCATCAGTACGCG 1020
DB 652 ValAlaValCysSerPheArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla 671
QY 1021 GCCCTGTGACCAAGACCAACCGCATTTACGGATCTTTGAGCAGGCGCAACGCTCGGTC 1080
DB 672 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysLysSerVal 691
QY 1081 AGTCCCCCGGCTTTTCATCAGCCCCCGCTCGCAGCTGGCCCATCACCTTCATCTCATCTCC 1140
DB 692 ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer 711
QY 1141 CTGAGCTGCTCGGCATCTCGGT 1200
DB 712 ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProProAsnIleIleIleAsp 731
QY 1201 TTCAGGACCAACGACACTTGACCCCGCTTTGCCAGGGCGGCTCAAGTGCAGATC 1260
DB 732 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 751

Qy	64	AGCCGCACGCTGGGACAAACAACAGCGCGCAACATCTGGTTTCCGAGTCTCTGGGAGGACAAAC	123
Db	352	SerArgThrLeuGluAAsnAenArgAAsnValTrpPheAlaGluTrpGluGluAAsn	371
Qy	124	TTCCATTGCCAAGTTGAGCCGCCACCGCTCAAGAAAGGAGCCACATCAAGAAGTGCACC	183
Db	372	PheAenCysIysLeuThrIleSerGlySerIysIysGluAspThrAspArgIysCysThr	391
Qy	184	AACCGCAGCGCATCTGGCGCAGGACTTCGGCCCTATCAGCAGGAGGGAAGTGCAGTTTCGTG	243
Db	392	GlyGlnGluArgIleGlyIysAspSerAsnTyrGlnGlnGluGlyIysValGlnPheVal	411
Qy	244	ATTGACGCTGTGTACGCATGGCCACGCGCTGCACGCCATGCACCGTACCTGTGTGCC	303
Db	412	IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAenIysAspLeuCysAla	431
Qy	304	GGCCGCGTAGGACTCTGCCCTCGCATCGGACCCCGTGGATGGCACCCAGCTGCTTAGTAC	363
Db	432	AspTyrArgGlyValCysProGluMetGlnAlaGlyGlyIysIysLeuLeuIysTyr	451
Qy	364	ATCAGGAACGTCAACTTCTCAGGCATTTCGGGGAAACCTCTTAACCTTTCATAGAACGGA	423
Db	452	IleArgHisValAenPheAenGlySerAlaGlyThrProValMetPheAenIysAenGly	471
Qy	424	GACGCACCGGGCGCTACGACATCTACAGTACCACTGCGCAAT---GGCTCGCGCGAG	480
Db	472	AspAlaProGlyAspTyrAspIlePheGlnTyrGlnThrThrAenThrThrAsnProGly	491
Qy	481	TACAAGTTCATCGCTCGTGGACAGACCACTGCACCTCAGATAGAGCGATGCAGTGG	540
Db	492	TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAenIleGluAspMetGlnTrp	511
Qy	541	CCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCCGGGAG	600
Db	512	GlyIysGlyValArgGluIleProSerSerValCysThrLeuProCysIysProGlyGln	531
Qy	601	CGAAAGAAGACTGTGAAGGGCATGGCTTGCTGTGGCACTGCGAGCCCTGCACCGGTAC	660
Db	532	ArgIysIysThrGlnIysGlyThrProCysCysIserTrpThrCysGluProCysAspGlyTyr	551
Qy	661	CAGTACCAAGTGGACCGCTACACCTGTAAAGACTGCCCTCAGNACATCGCGGCCACAG	720
Db	552	GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAenGlu	571
Qy	721	AACCGCAGAGCTGCCAGCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGCC	780
Db	572	AsnArgThrGlyCysGlnAenIleProIleIleIysLeuGlnTrpHisSerProItrPala	591
Qy	781	GTGCTGCCCTCTTCCTGGCGGTGGGACATCGCCGCCACGCTGTTGCTGGTGGTCAAG	840
Db	592	ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr	611
Qy	841	TTTGTCGCTACAAACGATATCCCCCATCGTCAGACCTCGGGCGCGGAACTGAGCTACG	900
Db	612	PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal	631
Qy	901	CTGCTGGCGGCATCTTCTGTGCTAGCCACATCTTCTCTCATGTATCGCAGAGCCGAC	960
Db	632	LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaIysProAsp	651
Qy	961	CTGGGACCTTTCCTCGCTCCGCGCATCTTCTTAGGGCTCGGCATGAGCATCAGCTACG	1020
Db	652	ValAlaValCysSerPheArgArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla	671
Qy	1021	GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGACGAGGCGCAACCGTTCG	1080
Db	672	AlaLeuLeuThrIysThrAsnArgIleTyrArgIlePheGluGlnGlyIysIysSerVal	691
Qy	1081	AGTGCCTGGCTTTCATGACCCCGCTCGCAGCTGGCGCATCACTTCATCTCATCTCC	1140
Db	692	ThrAlaProArgLeuIleIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer	711
Qy	1141	CTGCAGCTGCTCGGCATCTCGTGTGGTGTGGTGGACCCCTCCCACTCGGTGGTGGAC	1200

Db	712	VaIGlnLeuLeuGlyValPheIleTyrPheGlyValAspProProAsnIleIleIleAsp	731
Qy	1201	TTTCAGGACCAACGGACACTTGACCCCGCTTTCAGGGCGGTGCTCAAGTCGCGACATC	1260
Db	732	TyrAspGluHisIysThrMetAsnProGluGlnAlaArgGlyValLeuIysCysAspIle	751
Qy	1261	TCGGACCTGTCCTCATCTGCTGCTGGCTACAGCATGCTGCTGATGTCACGTGACT	1320
Db	752	ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr	771
Qy	1321	GTGTAGCCCATCAAGACCCGAGCGCTGCCGAGACCTTCACGAGGCCAAGCCCATCGGC	1380
Db	772	ValTyrAlaIleIysThrArgGlyValProGluAsnPheAsnGluAlaIysProIleGly	791
Qy	1381	TTACCATGTACACCACTGCTCATCTGCTGGCTTTCATCCCCATCTTTTGTGGCACC	1440
Db	792	PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThr	811
Qy	1441	TCACAGTCAGCCGACCAAGCTGTATCATCCAGACCAACACACTGACGGTCTCCGTGAGTCTG	1500
Db	812	AlaGlnSerAlaGluIysLeuTyrIleGlnThrThrThrLeuThrIleSerMetAsnLeu	831
Qy	1501	AGCGCTTCAGTTCCTCTGGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCAC	1560
Db	832	SerAlaSerValAlaLeuGlyMetLeuTyrMetProIysValTyrIleIleIlePheHis	851
Qy	1561	CCGAGCAGAACCTGCCCAAGCGCAGCGAGTCTCAAAGCCGTGTCAACCGCGGCACC	1620
Db	852	ProGluLeuAsnValGlnIysArgLysArgSerPheIysAlaValValThrAlaAlaThr	871
Qy	1621	ATGTCCAAACAGTTCACACAGAAGGGCAACTTCAGGCCCAATGGGAAGCCAAATCAGAG	1680
Db	872	MetSerSerArgLeuSerHisIysProSerAspArgProAsnGlyGluAlaIysThrGlu	891
Qy	1681	CTGTGTGAGAACTGGAGACCCCGCTGGCTTACCAACAGACCTTACGTCACCTACACC	1740
Db	892	LeuCysGluAsnValAspProAsnSerProAlaAlaIysIysIysTyrValSerTyrAsn	911
Qy	1741	AACCATGCCATC 1752	
Db	912	AsnLeuValIle 915	
RESULT 13			
Q8NFS2	1D	Q8NFS2	PRELIMINARY; PRT; 906 AA.
AC	Q8NFS2	AC	Q8NFS2; 2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002	DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-JUN-2003	DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Metabotropic glutamate receptor 7 variant 5.	DE	Metabotropic glutamate receptor 7 variant 5.
GN	Name=GRM7;	GN	Name=GRM7;
OS	Homo sapiens (Human).	OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa;	OC	Eukaryota; Metazoa;
OC	Mammalia; Eutheria;	OC	Mammalia; Eutheria;
OC	NCBI_TaxId=9606;	OC	NCBI_TaxId=9606;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	MEDLINE=22048149; PubMed=12052533; DOI=10.1016/S0304-3940(02)00306-3;	RX	MEDLINE=22048149; PubMed=12052533; DOI=10.1016/S0304-3940(02)00306-3;
RA	Schulz H.L., Stoehr H., Weber B.H.F.;	RA	Schulz H.L., Stoehr H., Weber B.H.F.;
RT	"Characterization of three novel isoforms of the metabotropic	RT	"Characterization of three novel isoforms of the metabotropic
RT	glutamate receptor 7 (GRM7)."	RT	glutamate receptor 7 (GRM7)."
FL	Neurosci. Lett. 326:37-40(2002).	FL	Neurosci. Lett. 326:37-40(2002).
DR	ENBL; AF458054; AAM47559.1; -.	DR	ENBL; AF458054; AAM47559.1; -.
DR	HSP; P23385; IEWK.	DR	HSP; P23385; IEWK.
DR	GO; GO:0016020; C:membrane; IEA.	DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.	DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.	DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPR001828; ANF receptor.	DR	InterPro; IPR001828; ANF receptor.
DR	InterPro; IPR000337; GPCR_Mgr.	DR	InterPro; IPR000337; GPCR_Mgr.
DR	InterPro; IPR000162; Mglu_receptor.	DR	InterPro; IPR000162; Mglu_receptor.
DR	InterPro; IPR001883; Mglu_receptor7.	DR	InterPro; IPR001883; Mglu_receptor7.
DR	InterPro; IPR011500; NCD3G GPCR.	DR	InterPro; IPR011500; NCD3G GPCR.

DR	Pfam; PF00003; 7cm_3; 1.
DR	Pfam; PF01094; ANF_receptor; 1.
DR	Pfam; PF07562; NCD3G; 1.
DR	PRINTS; PR00248; GPCRMR.
DR	PRINTS; PR01057; MTABOTROPCTR.
DR	PRINTS; PR00593; MTABOTROPICR.
DR	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR	PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR	PROSITE; PS02059; G_PROTEIN_RECEP_F3_4; 1.
KW	Receptor.
SQ	SEQUENCE 906 AA; 101301 MW; 53EC7BB83CBCB61 CRC64;

Alignment Scores:	
Pred. No.:	1.69e-122 Length: 906
Score:	2189.00 Matches: 401
Percent Similarity:	83.39% Conservative: 71
Best Local Similarity:	70.85% Mismatches: 92
Query Match:	66.27% Indels: 2
DB:	2 Gaps: 2

US-10-828-332-6 (1-1755) x Q8NFS2 (1-906)

Qy	7	GGGGTATCATCATCTTTGCCAACGGATGACA---TCAGSGTTCCACCGATACTTCTCC	63
Dd	332	GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaYrPheThr	351
Qy	64	AGCGCGACGTGGCAACAAACAGGGCGCAACATCTGGTTTGCCGAGTCTCGGAGGACAAAC	123
Dd	352	SerArgThrLeuGluLeuAsnArgAsnValTrpPheAlaGluYrTrpGluAsn	371
Qy	124	TTCATTGCAAGTTGAGCGCCGCACCGCTCAAGAAGGGGAAGCACATCAAGAAGTGCACC	183
Dd	372	PheAsnCylsLeuThriLeSerGlySerIlysGluAspThrAspArgIysCysThr	391
Qy	184	AACGAGAGCGCATCGGCGAGCACTCGGCTTATGACGAGGAGGAGGTGCACTTCGTG	243
Dd	392	GlyGlnGluArGIleGlyAspSerAsnTyrgluGlnGluGlyValGlnPheVal	411
Qy	244	ATTGACGCTGTGACGTCATGGCCACGCGTGCACGCATGCACCGTGCACCTGTGTCTCC	303
Dd	412	IleaspAlaValTyralaMetAlahisAlaLeuHisMetAsnIlyAspLeuCysAla	431
Qy	304	GGCCGCTGAGACTCTGCCCTCGCATGGACCCCGTGGATGGACCCAGCTGCTTAAGTAC	363
Dd	432	AspTyrgGlyValCysProgluMetGluGlnAlaGlyIlysIleLeuIlysrYr	451
Qy	364	ATCAGGAACGTCATCTTCAGGCATATCGGGGGAACCTGTAACTTCATGAGAACGGA	423
Dd	452	IleargAsnValAsnPheAsnGlySerAlaGlyThrProValImetPheAsnIlyAsnGly	471
Qy	424	GACSCACGGGGCGCTACGACATCTPACCAAGTACCAACTGCCGAANGGCTCG--GCCGAG	480
Dd	472	AspAlaProGlyArGtyrAspIlePheGlnTyrglnThrThrAsnThrSerAsnProGly	491
Qy	481	TACAAGGTTCATCGGCTCGTGACAGACACCACTGCACCTCAGAAATAGACGATGCAGTGG	540
Dd	492	TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp	511
Qy	541	CCAGGAGTGGCCAGCAGCTGCCCGCTCCATCTGCAGTCTGCCTCTGCCGCCCGGGGAG	600
Dd	512	GlyIysGlyValArgGluIleProAlaSerValCysThrLeuProCysIlysrProGln	531
Qy	601	CGAARGAGACTGTCAAGGCATGGCTTGCTGCTGGCACTGGCAGCCCTGCACCCGGTAC	660
Dd	532	ArgIlysrYsrThrGlnIlysrGlyThrProCysCysTrpThrCysGluProCysAspGly	551
Qy	661	CAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATGCGGCCACAGAG	720
Dd	552	GlnTyrglnPheAspGluMetThrCysGlnHisCysProTyraSpGlnArgProAsnGlu	571
Qy	721	AACCGCAGAGCTGCCGCCCATCCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGGCC	780

DE Metabotropic glutamate receptor 7 variant 4.
 GN Name=GRM7;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22048149; PubMed=12052533; DOI=10.1016/S0304-3940(02)00306-3;
 RT "Characterization of three novel isoforms of the metabotropic
 glutamate receptor 7 (GRM7).";
 RL Neurosci. Lett. 326:37-40(2002).
 DR EMBL; AF458053; AAM47558.1; -;
 DR HSP; P23385; 1EWK.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR000162; Metglu_receptor.
 DR InterPro; IPR001883; Metglu_receptor7.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCR_MGR.
 DR PRINTS; PR01057; MTABOTROPCTR.
 DR PRINTS; PR00593; MTABOTROPICR.
 DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
 KW Receptor.
 SQ SEQUENCE 911 AA; 101841 MW; 178DC0821EAD05B5 CRC64;

Alignment Scores:
 Pred. No.: 1,696-122 Length: 911
 Score: 2189.00 Matches: 401
 Percent Similarity: 83.39% Conservative: 71
 Best Local Similarity: 70.85% Mismatches: 92
 Query Match: 66.27% Indels: 2
 DB: 2 Gaps: 2

US-10-828-332-6 (1-1755) x QBNFS3 (1-911)

QY 7 GGGGTATCATCATCTTTCCACGAGGATGACA---TCAGGGTTCGACCGCATCTTCTCC 63
 DB 332 GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaTyrPheThr 351
 QY 64 AGCCGACGCTGGACAACACGAGGCGCAACATCTGTTTGGCGAGTTCTGGAGGACAC 123
 DB 352 SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTyrTrpGluAsn 371
 QY 124 TTCATTGCAAGTTGACGGCGCCACGCGCTCAAGAGGAGGACCATCAAGAGTGACAC 183
 DB 372 PheAsnCysLysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr 391
 QY 184 AACCGAGAGCGCATCGGCGAGGACTCGGCGCTATGACGAGGAGGAGGAGGAGTTCGTG 243
 DB 392 GlyGlnGluArgIleGlyLysAspSerAsnTyrGlnGlnGluGlyLysValGlnPheVal 411
 QY 244 ATTGACGCTGTAGCCCATGGCCACGCGGTGACGCGCATGACCGCTGCTGTGTCCTCC 303
 DB 412 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAsnLysAspLysCysAla 431
 QY 304 GSCCGGTAGGACTCTGCGCTCGCATGGACCCCGGTGGATGGCCACCGCTGCTTAAGTAC 363
 DB 432 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyLysLysLeuLeuLysTyr 451
 QY 364 ATCAGGAACGTCAACTTCTCAGGCATTCGGGGAAACCTGTAACTTCAATGAGAACCGGA 423
 DB 452 IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 471

QY 424 GACGACCGGGCGCTACGACATCTACAGTACCACAACTGCGCAATGCGCTCG---GCCGAG 480
 DB 472 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrThrAsnThrSerAsnProGly 491
 QY 481 TACAAGGTCAATCGCTCGTGGACAGACACCTGACCTCAGAAATAGAGCGGATGACAGTGG 540
 DB 492 TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 511
 QY 541 CCAGGGAGTGGCCAGCAGCTGCGCGCTCCATCTGAGTCTGCGCTCCAGCCCGGGGAG 600
 DB 512 GlyLysGlyValArgGluIleProAlaSerValCysThrLeuProCysLysProGlyGln 531
 QY 601 CGAAAGAAGACTGTGAAGGCGATGGCTTGTCTGCGCACTGCGAGCCCTGCACCGGGTAC 660
 DB 532 ArgLysLysThrGlnLysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr 551
 QY 661 CAGTACCAGTGGACCGCTACACCTGTAAAGACCTGCCCCCTACGATGCGGCGCCACAGAG 720
 DB 552 GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu 571
 QY 721 AACCGCAGAGCTGCGCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGTGGGCC 780
 DB 572 AsnArgThrGlyCysGlnAspIleProIleLysLeuGluTrpHisSerProTrpAla 591
 QY 781 GTGCTGCCCTCTTCTGCGCGTGGTGGCATCGCCGCGCTGTTCTGTTGGTGGTCCACG 840
 DB 592 ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr 611
 QY 841 TTTGTGCGCTACAACGATACCCCATCGTCAAGCGCTCGGCGCGGAACTAGTACGTG 900
 DB 612 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 631
 QY 901 CTGCTGCGGCGCATCTTCTGCTAGCCACCTACCTTCTCATGATCGGAGCCCGGAC 960
 DB 632 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 651
 QY 961 CTGGGACCTGTTCTGCTCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGCTAGCG 1020
 DB 652 ValAlaValCysSerPheArgArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla 671
 QY 1021 GCCCTGTGACCAAGACCAACCGCATTTACCGCATTTTGGAGCGGCGGCAACGTCGCTC 1080
 DB 672 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysLysSerVal 691
 QY 1081 AGTCCCGCGGTTTCATCAGCCCGCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCC 1140
 DB 692 ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer 711
 QY 1141 CTGACGCTGCTCGGCATCTGCGTGGTGGTGGTGGACCCCTCCCACTCGGTGGTGGAC 1200
 DB 712 ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProProAsnIleIleAsp 731
 QY 1201 TTCAGGACCAACGACACCTTGACCCCGCTTTGCCAGGCGCGTCTCAAGTGGACATC 1260
 DB 732 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 751
 QY 1261 TCAGACCTGTCCCTCATCTGCGCTGAGCATGCTGCTGATGCTGCTGATGCTGCTGCTG 1320
 DB 752 ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr 771
 QY 1321 GTGTACCCCATCAAGACCCGAGGCGTCCGAGACCTTCAACGAGGCGCAACCCCATCGGC 1380
 DB 772 ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly 791
 QY 1381 TTCACCATGTACACCACTGCATTTGTGCTGGCTGCCTTCATCCCATCTTTTGGGACCC 1440
 DB 792 PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr 811
 QY 1441 TCACAGTCAGCGCAGAGCTGTATCATCCAGACACCATCAGCGGTCTCCGTGAGTGTG 1500
 DB 812 AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrLeuThrIleSerMetAsnLeu 831

Qy	1501	AGCGCTTCAGTGTCCTCGGGGATGCTCTACATGCCCAAAGCTCTACATCATCTCTCTCTCCAC	1560
Db	832	SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIleIleIlePheHis	851
Qy	1561	CCGGAGCAGAACGTGGCCCAACGCCGACGAGTCTCAAAGCCGTGGTCACCGCGCGCAC	1620
Db	852	ProGluLeuAsnValGlnLysArgLysArgSerPheLysAlaValThrAlaAlaThr	871
Qy	1621	ATGTCCCAACAGTTTCACACAGAGGGCAACTCAGCGCCCAATGGGGAAGCCAAATCAGAG	1680
Db	872	MetSerArgLeuSerHisHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu	891
Qy	1681	CTGTGTCAGAACCTGGAG	1698
Db	892	LeuCysGluAsnValAsp	897

RESULT 15

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AC QNFNS4      PRELIMINARY;      PRPT;      924 AA.
AD AC          QNFNS4;
DT 01-OCT-2002 (TREMBlRel. 22, Created)
DT 01-OCT-2002 (TREMBlRel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlRel. 24, Last annotation update)
DE Metabotropic glutamate receptor 7 variant 3.
GN Name=GRM7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
RP MEDLINE=22048149; PubMed=12052533; DOI=10.1016/S0304-3940(02)00306-3;
RX Schulz H.L., Stoehr H., Weber B.H.F.;
RT "Characterization of three novel isoforms of the metabotropic
RT glutamate receptor 7 (GRM7)";
RL Neurosci. Lett. 326:37-40(2002).
DR EMBL; AF458052; AAM47557.1; -.
DR HSP; P23385; IEWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mglu_receptor.
DR InterPro; IPR001883; Mglu_receptor7.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR01057; MTABOTROPC7R.
DR PRINTS; PR00593; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
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SQ SEQUENCE.      924 AA; 103375 MW; 32028B6156A71BFE CRC64;

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Qy 1201 TTCAGGACCAACGGACACTTGACCCCGCTTGGCAGGGCGGTGCTCAAGTGGACATC 1260
Db 732 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 751
Qy 1261 TCGGACCTGTCCCTCATCTGCTGGCTGCTACAGCATGCTGCTGATGGTCACGTGTACT 1320
Db 752 ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr 771
Qy 1321 GTGTACGCCATCAAGACCGAGCGGTGCCCGAGACCTTCAACGAGGCCCAAGCCCATCGGC 1380
Db 772 ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly 791
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Db 892 LeuCysGluAsnValAsp 897
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Search completed: June 17, 2005, 18:51:06
Job time : 367.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 17, 2005, 18:27:32 ; Search time 67 Seconds
(without alignments)
5040.610 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 3303

Sequence: 1 atgcacgggggtatcatcatc.....acaccaaccatgcctatctag 1755.

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-O=/cgn2_1/USPTO_spool_p/US10828332/runat_17062005_171336_24962/app_query.fasta_1.1927
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -MODE=LOCAL
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10828332@cgn 1 1.92 @runat_17062005_171336_24962 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3050.5	92.4	912	2 JH0563	metabotropic gluta
2	2336	70.7	908	2 I49142	metabotropic gluta
3	2210	66.9	915	2 A49874	metabotropic gluta
4	2111.5	63.9	551	2 T30806	metabotropic gluta
5	2026.5	61.4	871	2 A46742	metabotropic gluta
6	1171.5	35.5	872	2 JH0561	metabotropic gluta
7	1155.5	35.0	879	2 JC7160	metabotropic gluta
8	1152.5	34.9	879	2 JH0562	metabotropic gluta
9	1123	34.0	1180	2 JC2132	metabotropic gluta
10	1123	34.0	1212	2 JC2131	metabotropic gluta
11	1122	34.0	1199	2 A41939	G protein-coupled
12	1121	33.9	1171	2 A42916	metabotropic gluta
13	1114.5	33.7	1218	2 T71376	glutamate receptor
14	989.5	30.0	999	2 T27628	hypothetical prote

15	871.5	26.4	1267	2 T21340	hypothetical prote
16	691	20.9	1079	2 I59362	calcium/polyvalent
17	683	20.7	1085	2 S40476	Ca(2+)-sensing rec
18	679	20.6	1078	2 A56715	calcium receptor (
19	671	20.3	1088	2 B56715	calcium receptor (
20	308.5	9.3	858	2 JC7683	taste receptor T1R
21	308.5	9.3	1099	2 T16283	hypothetical prote
22	307.5	9.3	1367	1 S48478	glucan 1,4-alpha-g
23	299	9.1	3570	2 T45025	mucin MUC5B, trach
24	281.5	8.5	507	2 T44768	antifreeze glycope
25	278.5	8.4	528	2 I47141	gastric mucin (Glo
26	269.5	8.2	867	2 T45463	membrane glycoprot
27	268	8.1	866	2 T45462	membrane glycoprot
28	259	7.8	797	1 VGBEX1	glycoprotein X pre
29	258.5	7.8	2232	2 T34434	hypothetical prote
30	254	7.7	660	1 QQB33	BHLPI protein - hu
31	250.5	7.6	1032	2 T34433	hypothetical prote
32	245.5	7.4	1952	2 T48814	hypothetical prote
33	241.5	7.3	543	2 S35047	hypothetical prote
34	235	7.1	4776	2 E95206	mucin JUL7 - human
35	232.5	7.0	3020	2 A43932	cell wall surface
36	227.5	6.9	1106	2 JQ0405	mucin 2 precursor,
37	218.5	6.6	960	2 JE0356	hypothetical 119.5
38	216	6.5	1459	2 T32271	gamma-aminobutyric
39	214	6.5	580	2 T43481	hypothetical prote
40	212.5	6.4	784	2 JQ0317	probable mucin DXF
41	210.5	6.4	1970	1 S21054	hypothetical 82K p
42	210.5	6.4	1970	2 I38186	DNA-directed RNA p
43	209.5	6.3	383	2 T46707	RNA polymerase II
44	207.5	6.3	610	2 S35049	proteophosphoglyca
45	207.5	6.3	839	2 T04859	mucin JER57 - huma
					extensin homolog F

ALIGNMENTS

RESULT 1

JH0563 metabotropic glutamate receptor 4 precursor - rat.

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: JH0563; I58149

R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.

Neuron 8, 169-179, 1992

A>Title: A family of metabotropic glutamate receptors.

A:Reference number: JH0561; MUID:92110002; PMID:1309649

A:Accession: JH0563

A:Molecule type: mRNA

A:Residues: 1-912 <TAN>

A:Cross-references: UNIPROT:P31423

A:Experimental source: brain

R:O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.; McGrane, V.,

Neuron 11, 41-52, 1993

A>Title: The ligand-binding domain in metabotropic glutamate receptors is related to bac

A:Reference number: I58149; MUID:93332699; PMID:8338667

A:Accession: I58149

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-123 'R', 125-912 <RES>

A:Cross-references: GB:M90518; NID:g205400; PIDN:AA93190.1; PID:g205401

C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m

C:Genetics:

A:Gene: GLUR4

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F:1-32/Domain: signal sequence #status predicted <SIG>

F:33-912/Product: metabotropic glutamate receptor 4 #status predicted <TRI>

F:588-610/Domain: transmembrane #status predicted <TRI>

F:625-645/Domain: transmembrane #status predicted <III>

F:657-675/Domain: transmembrane #status predicted <III>

F:700-720/Domain: transmembrane #status predicted <IV>

F:751-772/Domain: transmembrane #status predicted <TRV>

F:786-807/Domain: transmembrane #status predicted <TVI>

F:822-847/Domain: transmembrane #status predicted <VII>

F:98,301,454,484,569/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted

Alignment Scores:

Pred. No.: 6,53e-191 Length: 912
Score: 3050.50 Matches: 575
Percent Similarity: 98.97% Conservative: 2
Best Local Similarity: 98.63% Mismatches: 5
Query Match: 92.36% Indels: 1
DB: 2 Gaps: 1

US-10-828-332-6 (1-1755) x JH0563 (1-912)

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QY 7 GGGGTATCATCTTCCACAGGAGGATGACA---TCAGGGTTCGACCGATCTTCTCC 63
DB ::::|
330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349

QY 64 AGCCGACGCTGGACAAACAGGCGCAACATCTGTTTTCGAGATTTCTGGAGAGCAAC 123
DB ::::|
350 SerArgThrLeuAspAsnAsnArgAsnIleTyrPheAlaGluPheTrpGluAspAsn 369

QY 124 TTCATTGCAAGTTGAGCGGCACGCGCTCAAGAGGGAAGCCACATCAAGAAGTGCACC 183
DB ::::|
370 PheHisCysLeuSerArgHisAlaLeuLysLysGlySerHisIleLeuLysCysThr 389

QY 184 AACCGAGAGCCGCTCGGACGACTCGCGCTATGACGAGGAGGGAAGTGCAGTTCGTG 243
DB ::::|
390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409

QY 244 ATTGACGCTGTGTACGCCATGGCCACGCGCTGCACGCGCATGACCGTGACTGTGTC 303
DB ::::|
410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCyBPro 429

QY 304 GGCCTGCTAGGACTGTCCTCGCATGCAACCCGCTGGATGCAACCCAGTCTCTTAAGTAC 363
DB ::::|
430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449

QY 364 ATCAGGACGTCNACTTCTCAGGCAATTCGGGGACCCCTGTAACTTCAATGAGACGGA 423
DB ::::|
450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469

QY 424 GACGACCGGGCGCTACGACATCTACCACTACCACTGCGCAATGCTCGCGCGAGTAC 483
DB ::::|
470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 489

QY 484 AAGTTCATCGCTCTGTGACAGACCACTGCACTCAGAAATAGACGCGATGCGGCA 543
DB ::::|
490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 509

QY 544 GGGAGTGGCCAGCAGCTCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCCGGGAGCGA 603
DB ::::|
510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529

QY 604 AAGAGACTGTGAAGGCGATGCTGTGCTGGCACTCGGAGCCCTGCACCGGGTACCAG 663
DB ::::|
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QY 664 TACCAGTGGACCGCTACACCTGTGAAGACCTGCGCCCTACGACATGCGGCCCCACAGAAC 723
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QY 724 GCGCAGACTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGAGTGGCGGCGGTG 783
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570 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 589

QY 784 CTGCCCTCTTCTCGCGCTGTGGCGCATCGCGCGACGCTGTTCTGCTGGTGGTCACTTT 843
DB ::::|
590 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 609

QY 844 GTGCGCTACAAGTACCCCATCTCAAGGCTCGGCGCGGGAAGTCAAGTCACTGCTGTG 903
DB ::::|
610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
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QY 904 CTGCGCGGCGCTCTTCTGTGTCTACGCGCACTACCTTCTCTCATGTCGAGACCGGACCTG 963
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QY 964 GGGACCTGTTCTGCTCCCGCGCATCTTCTTAGGGCTCGGATGAGCATCAGCTACGCGGCC 1023
DB ::::|
650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669

QY 1024 CTGCTGACCAAGACCAACCGCATTTACCGCATCTTTCAGAGGAGCAACCGTCCGTCAGT 1083
DB ::::|
670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689

QY 1084 GCCCGCGTTCATCAGCGCGGCTCGCAGCTGGCCATCACCTTCTCATCTCTCCCTG 1143
DB ::::|
690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 709

QY 1144 CAGTGTCTCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1203
DB ::::|
710 GlnLeuLeuGlyIleCysValTyrPheValValAspProSerHisSerValValAspPhe 729

QY 1204 CAGGACCAACGGACACTTGACCCCGCTTTGCCAGGGCGTGTCTCAAGTGCACATCTCG 1263
DB ::::|
730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749

QY 1264 GACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
DB ::::|
750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769

QY 1324 TAGCCCATCAAGACCCGAGCGGTGCGGAGACCTTCAACGAGGCGCAAGCCCATCGGCTTC 1383
DB ::::|
770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789

QY 1384 ACCATGTACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
DB ::::|
790 ThrMetTyrThrThrCysIleValTyrPheAlaPheIleProIlePhePheGlyThrSer 809

QY 1444 CAGTCACCGCAAGCTGTATCATCCAGAACACACACTGACGGTCTCCGTGAGTCTCAGC 1503
DB ::::|
810 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 829

QY 1504 GCTTCAGTGTCCCTGGGATGCTCTACATGCCCCAAAGTCTACATCATCTCTTCCACCCG 1563
DB ::::|
830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro 849

QY 1564 GAGCAGACCTGCGCCAGCGCAGCGCTCAAAAGCGTGTCCAGCGCGCCACCATG 1623
DB ::::|
850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 869

QY 1624 TCCAAACAGTTTCAACAGAGGCGCACTTCAGGCGCCCAATGGGGAAGCCAAATCAGAGCTG 1683
DB ::::|
870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889

QY 1684 TGTGAGAACCTGGAGACCCCGCTGCTACCAAGACCTACCAAGACCTACCTACCAAC 1743
DB ::::|
890 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 909

QY 1744 CATGCCATC 1752
DB ::::|
910 HisAlaIle 912

RESULT 2
149142
metabotropic glutamate receptor 8 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49142
R:Duvoisin, R.M.; Zhang, C.; Ramonell, K.
J. Neurosci. 15, 3075-3083, 1995
A:Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory
A:Reference number: 149142; MUID:95239344; PMID:7722646
A:Accession: I49142
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
```

A;Residues: 1-908 <RES>
A;Cross-references: UNIPROT:P47743; EMBL:U17252; NID:G854728; PID:AAA68149.1; PID:G854728
C:Genetics:
A;Gene: mGluR8
C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: neurotransmitter receptor

Alignment Scores:		
Pred. No.:	2,18e-144	Length: 908
Score:	2336.00	Matches: 432
Percent Similarity:	84.39%	Conservative: 60
Best Local Similarity:	74.10%	Mismatches: 89
Query Match:	70.72%	Indels: 2
DB:	2	Gaps: 2

US-10-828-332-6 (1-1755) x I49142 (1-908)

Qy	7	GGGGTATCATCATCTTTGGCAACGAGGATGACA---TCAGGGTTGCACGCACTACTTCTCC	63
Db	327	GlyAlaValThrIleLeuProLysArgAlaSerIleAspGlyPheAspArgTyrPheArg	346
Qy	64	AGCGCAGCGTGGACACAACAAGCGGCAACATCTGTTTCCGAGTTCGGGAGGACAAC	123
Db	347	SerArgThrLeuAlaAsnArgAenValTrpPheAlaGluPheSerGluGlyAen	366
Qy	124	TTCCATTGCAAGTTCAGCGCCACGCGCTCAAGAAGGGAAGCCACATCAAGAAGTGCACC	183
Db	367	PheGlyCysLysSerGlySerHisGly--LysArgAenSerHisIleLysLysCysThr	385
Qy	184	AACGAGAGCGCATCGGCAGAGACTCGGCCTATAGACAGAGGGAGGTGCATTCGTG	243
Db	386	GlyLeuGluArgIleAlaArgAspSerTyrGluGlnGluGlyLysValGlnPheVal	405
Qy	244	ATTGACGCTGTAGCGCATGGCCACGCGCTGCACGCCATGCACCGTCACCTGTCTCC	303
Db	406	IleAspAlaValTyrSerMetAlaTyrAlaLeuHisAsnMetHisLysGluLeuCysPro	425
Qy	304	GGCGCGTGGACTCTGCCTCGCATGAGACCCGCTGGATGGCACCCAGCTGCTTAAGTAC	363
Db	426	GlyTyrIleGlyLeuCysProArgMetValThrIleAspGlyLysGluLeuLeuGlyTyr	445
Qy	364	ATCAGGAACGCTCAACTCTCAGGCATTCGGGGACCCCTGTAACTTCAATCAGACGCA	423
Db	446	IleArgAlaValAsnPheAsnGlySerAlaGlyThrProValThrPheAsnGluAenGly	465
Qy	424	GACGACCGGGCGCTACGACATCTACCAAGTACCAACTCGCGCAATGGCTCGCGCCGATAC	483
Db	466	AspAlaProGlyArgTyrAspIlePheGlnTyrGlnIleAsnAsnLysSerThrGluTyr	485
Qy	484	AAGTTCATCGGCTCGTGACAGACACCACTGCACCTCAGCAATAGACGGATGAGTGCCA	543
Db	486	LysIleIleGlyHisIleTrpThrAsnGlnLeuHisLeuLysValGluAspMetGlnTrpAla	505
Qy	544	GGGAGTGGCCAGCAGCTCGCGGCTCCATCTCCAGTCTGCCTTCGCGAGCCGGAGGCA	603
Db	506	AsnArgGluHisThrHisProAlaSerValCysSerLeuProCysIleProGlyLysGluArg	525
Qy	604	AAGAAGACTGTGAAGGCGATGGCTTGCTGTGGCACTGCGAGCCCTGCACCGGTACCAAG	663
Db	526	LysLysThrValLysGlyValProCysCysIleTrpHisCysGlyArgCysGluGlyTyrAen	545
Qy	664	TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATCGGCGCCACAGNAC	723
Db	546	TyrGlnValAspGluLeuSerCysGluLeuCysProLeuAspGlnArgProAsnIleAen	565
Qy	724	CGCACGAGCTGCCAGCCCATCCCACTCGTCAAGTTGGAGTGGGACTCGCGCTGGCGCGTG	783
Db	566	ArgThrGlyCysArgIleProIleIleLysLeuGluTrpHisSerProIleValVal	585
Qy	784	CTGCCCTCTTCCTGGCGGTGGGCAATCGCCCGCCACGCTCTTGTGTGTGTGTGTGTGT	843
Db	586	ValProValLeuIleAlaIleLeuGlyIleIleAlaThrThrPheValIleValThrPhe	605

RESULTS

metabotropic glutamate receptor 7 - rat
N; Alternate names: metabotropic glutamate receptor mGluR7
C; Species: Rattus norvegicus (Norway rat)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_02-Jul-1996
C; Accession: A49874; 157954
R; Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R. *Biol. Chem.* 269, 1231-1236, 1994.

A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coup
A:Reference number: A49874; MUID:94117433; PMID:8288585
A:Accession: A49874
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA

A:Residues: 1-915 <RES>
A:Cross-references: UNIPROT:P35400; GB:D16817; NID:9458728; PIDN:BA040492.1; PID:g458729
R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.
Mol. Pharmacol. 45: 367-372, 1994
A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid
A:Reference number: I57954; MUID:94195260; PMID:8145723
A:Accession: I57954
A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA
A:Residues: 1-915 <RE2>
A:Cross-references: EMBL:U06832; NID:9459657; PIDN:AAA20655.1; PID:g459658

C:Genetics:

A:Gene: MGLUR7

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: neurotransmitter receptor

Alignment Scores:
Pred. No.: 3.49e-136 Length: 915
Score: 2210.00 Matches: 406
Percent Similarity: 82.53% Conservative: 76
Best Local Similarity: 69.52% Mismatches: 100
Query Match: 66.91% Indels: 2
DB: 2 Gaps: 2

US-10-828-332-6 (1-1755) x A49874 (1-915)

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QY 7 GGGGTATCATCATCTTCCGACGAGGATGACA---TCAGGGTTCGACCGATACTTCTCC 63
DB 332 GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaTyrPheThr 351
QY 64 AGCCGACGCTGGACAAACAGGCGCAACATCTGGTTTGGCGAGTTCTGGGAGACAAAC 123
DB 352 SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTyrTrpGluGluAsn 371
QY 124 TTCATATGCAAGTTGAGCGCCGACCGCTCAAGAAGGAGGACCATCAAGAAGTGACAC 183
DB 372 PheAsnCysLysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr 391
QY 184 AACCGAGAGCGATCGGCGAGACTCGGCCTATGACGAGGAGGAGGAGGAGTGCAGTTCGTG 243
DB 392 GlyGlnGluArgIleGlyLysAspSerAsnTyrGluGlnGluGlyLysValGlnPheVal 411
QY 244 ATTGACGCTGTGTACGCCATGGCCGACGCTGCACCGCATCGACCGTGTGTCTCC 303
DB 412 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAsnLysAspLeuCysAla 431
QY 304 GCGCGGTAGGACTCTGCCCTCGCATGGACCCCGTGGATGGACCCGACTGCTTAAGTAC 363
DB 432 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyLysLysLeuLeuLysTyr 451
QY 364 ATCAGGACGCTCACTTCTGAGGCAATCGGGGACCTGTAACTTCAATGAGACGACGA 423
DB 452 IleArgHisValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 471
QY 424 GACGACCGGGCGCTACGACATCTACACGATACCACTCGCGCAAT---GGCTCGCGCCGAG 480
DB 472 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrAsnThrThrAsnProGly 491
QY 481 TACAAGGTATCGGCTCGTGGACAGACCACTGCACCTCAGAAATAGACGGATGACAGTGG 540
DB 492 TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 511
QY 541 CCAGGAGTGGCGACGAGTGGCGGCTCCATCTCAGTCTGCTGCTGCGAGCCCGGGGAG 600
DB 512 GlyLysGlyValArgGluIleProSerValCysThrLeuProCysLysProGlyGln 531
QY 601 CGAAGAAGACTGTGAAGGGCATGGCTGCTGCTGCGCATCGAGCCCTGCACCGGGTAC 660
DB 660
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DB 532 ArgLysLysThrGlnLysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr 551
QY 661 CAGTACCAAGTGGACCGCTACACTGTAAAGACCTGCGCCCTACGACATGCGGCCACACAG 720
DB 552 GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu 571
QY 721 AACCGACGAGCTGCCAGCCCCATCCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGGCC 780
DB 572 AsnArgThrGlyCysGlnAsnIleProIleIleLysLeuGluTrpHisSerProTyrAla 591
QY 781 GTGTGCGCCCTCTTCTTGGCGGTGGGATGCCCGCAGCTGTTGTTGTTGTTGTTGTTGTTG 840
DB 592 ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr 611
QY 841 TTTGTGCGCTACACGATACCCCATCGTCAAGSCCTCGGCGGGAACCTGAGCTACGCTG 900
DB 612 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 631
QY 901 CTGTGCGGGGATCTTTCTGTGTGTACGCCACTCTCTCATGATCGCAGAGCCGGAC 960
DB 632 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 651
QY 961 CTGGGAGCTGTGCTGCCCGCATCTTCTAGGGCTCGGCATGAGCATCAGTACGCG 1020
DB 652 ValAlaValCysSerPheArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla 671
QY 1021 GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGCAACGTCGTC 1080
DB 672 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysLysSerVal 691
QY 1081 AGTCCCGCGGTTTTCATCAGCCCGGCTCGCAGCTGGCCCATCCTTCTCATCTCTCC 1140
DB 692 ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer 711
QY 1141 CTGAGCTGTCTCGCATCTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
DB 712 ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProProAsnIleIleAsp 731
QY 1201 TTCAGGACCAACGACACTTGACCCCGCTTTGCCAGGGCGTCTCAAGTCGACATC 1260
DB 732 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 751
QY 1261 TCGACCTGTCTCTCATCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
DB 752 ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr 771
QY 1321 GTGTACGCCATCAAGACCCGAGGGTGTCCGAGACCTTCAACGAGGCGCAACCCATCGGC 1380
DB 772 ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly 791
QY 1381 TTCACCATGTACACCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
DB 792 PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr 811
QY 1441 TCACAGTCAGCCGACAAAGCTGTATCATCCAGACCAACACACTGACGGTCTCCGTGATCTG 1500
DB 812 AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrThrLeuThrIleSerMetAsnLeu 831
QY 1501 AGCGCTTCAAGTGTCCCTGGGATGCTCTACATGCCCAAGTCTATCATCATCTCTTCCAC 1560
DB 832 SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIlePheHis 851
QY 1561 CCGGAGCAGACGCGCCCAAGCGACGATCTCAAGCGGTGGTTCACCGCGCCGAC 1620
DB 852 ProGluLeuAsnValGlnLysArgLysSerPheLysAlaValThrAlaAlaThr 871
QY 1621 ATGTCCAAACAGTTTACACAGAAAGGCAACTTTCAGGCGCCCAATGGGGAAGCAATACAG 1680
DB 872 MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu 891
QY 1681 CTGTGTGAGAACCTGGAGACCCCGCGCTGGTGTACCAACAGACCTAGCTACCTACAC 1740
DB 892 LeuCysGluAsnValAspProAsnSerProAlaAlaLysLysTyrValSerTyrAsn 911
```

QY 1741 AACCATGCCATC 1752
DB 912 AsnLeuValIle 915

RESULT 4
T30806

metabotropic glutamate receptor 7 - Fugu rubripes (fragment)
C:Species: Fugu rubripes
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T30806
R: Cottage, A.J.; Clark, M.; Hawker, K.; Umrana, Y.; Wheller, D.; Bishop, M.; Elgar, G.
PDBS Lett. 443, 370-374, 1999
A: Title: Three receptor genes for plasminogen related growth factors in the genome of th
A: Reference number: Z08080; MUID: 99148833; PMID: 10025966
A: Accession: T30806
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-551 <COT>
A: Cross-references: UNIPROT: Q9PWQ0; EMBL: AJ010317; NID: e1355235; PID: e1355236; PIDN: CAAC
C: Genetics:
A: Gene: GRM7
A: Note: intron positions not resolved (incomplete sequence)
C: Superfamily: metabotropic glutamate receptor 4

Alignment Scores:
Pred. No.: 8,79e-130 Length: 551
Score: 2111.50 Matches: 376
Percent Similarity: 83.88% Conservative: 82
Best Local Similarity: 68.86% Mismatches: 87
Query Match: 63.93% Indels: 1
DB: 2 Gaps: 1

US-10-828-332-6 (1-1755) x T30806 (1-551)

QY 46 TTCGACCGACTACTCTCCAGCCGACGCTCGGCAACAAACAGGCGCAACATCTGGTTTCCC 105
DB 1 PheAapGlnTyrPheThrSerAgsSerLeuGluAsnAsnArgAGsnlleTrpPheala 20
QY 106 GAGTTCTGGGAGACAACCTTCCATTGCACTTGAGCCGCCACCGCTCAAGAGGGAAAGC 165
DB 21 GluPheTrpGluAaspAaspPheLysCysLysLeuThrArgProGlyIleLysTyrGluLeu 40
QY 166 CACATCAAGAAGTCACCAACCCAGAGCGCATGGGCGAGCTCGGCTATGACGAGAG 225
DB 41 GlyArgArgLysCysThrGlyAaspGluArgLysSerAaspSerGlnTyrGluGlnGlu 60
QY 226 GGGAAAGTGCAGTTCCTGATTGACGTGTGTAGCCCATGGGCCACCGGCTCGACGCCATG 285
DB 61 GlyLysValGlnPheValIleAaspAlaValTyrAlaMetAlaHisAlaLeuHisSerMet 80
QY 286 CACCGTGACCTGTGTCGGCCGCGTAGGACTCTGCCCTCGCATGAGACCCCGTGGATGC 345
DB 81 HisThrAaspLeuCysProGlySerMetGlyValCysAaspLysMetAaspProValGluGly 100
QY 346 ACCCAGCTGCTTAAGTACATCAGGAACGTCACTTCTCAGGCATTGCGGGGAACCCCTGTA 405
DB 101 ArgMetLeuLeuGlnTyrIleHisGlyValAsnPheAsnGlySerAlaGlyThrGlyVal 120
QY 406 ACCTTCAATGAGACCGAGACGCAACCGGGCGCTTACGACATCTACCAAGTACCAACTGC 465
DB 121 MetPheAsnGluAsnGlyAaspAlaProGlyArgTyrAaspIlePheGlnTyrGlnMetSer 140
QY 466 AAT----GGCTCGGCCGAGTACAAGTATCTCGGCTCTGGGACAGACCACTGCACCTCAGA 522
DB 141 AsnIleSerAsnProGlyTyrArgAsnIleGlyGlnTrpThrAsnHisLeuArgLeuAsn 160
QY 523 ATAGAGCGGATGCAAGTGGCCAGGAGTGGCCAGCAGCTCGCGCTCCATCTGAGTCTG 582
DB 161 LeuGluGluMetGlnTrpSerGlyGlyAaspArgLysIleProGluSerValCysSerPhe 180
QY 583 CCCTCCCAAGCCCGGAGGAGCAAGAGACTGTGAAGGGCATGCTTCTGCTGGCACTGC 642

Db	181	ProCysGluSerGlyGluArgLysLysMetValLysGlyValProCysCysTrpHisCys	200
Qy	643	GAGCCCTGCACCGGTACCAAGTGGACCGCTACACCTGTAGACCTGCCCTAC	702
Db	201	GlulLeuCysAspGlyTyrGlnTyrLeuLeuAspGluPheThrCysAspMetCysProTyr	220
Qy	703	GACATGGCGGCCACAGAAACCGCAGCGATGGCCGCCATCCCATCGTCAAGTTGGAG	762
Db	221	AspMetArgProLeuLysAsnArgThrGlyCysArgProThrProIleLysLeuGlu	240
Qy	763	TGGAGATCGCGGTGGCGTGGCCCTCTCTCGTGGCGTGGTGGGCATCGCGCCACG	822
Db	241	TrpSerSerProThrAlaIleIleProValPheLeuAlaIleLeuGlyIleLeuAlaThr	260
Qy	823	CTGTTCCTGTGTGCATCGTTTGTGGCTACAACGATACCCCATCGTCAAGGCTCGGGC	882
Db	261	ThrGlyValIleAlaThrPheIleArgPheAsnAspThrProIleValArgAlaSerGly	280
Qy	883	CGGGAATGAGTACGTGTCTGTGGCGGGCATCTTCTGTGTCTACGCCACTACTCTCTC	942
Db	281	ArgGluLeuSerTyrValLeuLeuThrGlyIlePheLeuIleTyrLeuIleThrPheLeu	300
Qy	943	ATGATCGCAGCGCGCATCTGGTTCCTCGCGCATCTCTCTAGGCGTGGC	1002
Db	301	MetIleAlaGluProSerAlaValAlaValCysAlaPheArgLeuPheLeuGlyLeuGly	320
Qy	1003	ATGAGCATCAGTACCGCGCCCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGAG	1062
Db	321	MetCysIleSerTyrSerAlaMetLeuThrLysThrAsnArgIleTyrArgIlePheGlu	340
Qy	1063	CAGGGCAACCGTCTGAGTGCCTCCCGGTTTCATCAGCCCGCGCTCGCAGCTGGCCATC	1122
Db	341	GlnGlyLysLysSerValThrProProLysPheIleSerProThrSerGlnLeuIleIle	360
Qy	1123	ACCTTCATCTCATCTCCCTGCGAGCTCTCGGCATCTGCGTGTGGTTCGTGGTGGACCCC	1182
Db	361	ThrPheIleLeuIleSerValGlnLeuLeuGlyValPheIleTrpPheGlyValMetPro	380
Qy	1183	TCCCACTCGGTGTGATCTCCAGGACCAACGACACTTGACCCCGCTTGCACGCGGC	1242
Db	381	ProHisThrIleIleAspTyrGluGluGlnLysProAsnProGluPheAlaArgGly	400
Qy	1243	GTGCTCAAGTGCACATCTCGGACCTGTCCCTCATCTGCTGTGGCTACAGCATGCTG	1302
Db	401	ValLeuLysCysAspMetSerAspLeuSerLeuIleLeuCysLeuSerTyrSerLeuVal	420
Qy	1303	CTGATGTCAGTGTACTGTGTAGCGCATCAAGCCGAGGCGTGCAGAGACTTCAAC	1362
Db	421	LeuMetIleThrCysThrValTyrAlaIleLysSerArgGlyValProGluThrPheAsn	440
Qy	1363	GAGCCAAAGCCATCGCTTACCATGTACACCACTGCATCTCTGGCTGGGCTTTCATC	1422
Db	441	GluAlaLysProIleGlyPheThrMetTyrThrThrCysIleValTrpLeuAlaPheVal	460
Qy	1423	CCCATCTTTTGGCACCTCACAGTCAGCCGACCAAGCTGTACATCCAGACCAACACACTG	1482
Db	461	ProIlePhePheGlyThrAlaGlnSerThrGluLysMetPheIleGlnThrThrLeu	480
Qy	1483	ACGGTCTCGTGTAGTCTGAGCGGCTTCAGTGTCTCCCTGGGATGTCTACATGCCCAAGTC	1542
Db	481	ThrValSerMetSerLeuSerAlaThrValSerLeuGlyMetLeuTyrIleProLysVal	500
Qy	1543	TACATCATCTCTTCCACCGGAGACAGCTGCCCAAGCGGACGAGCTCTCAAGGC	1602
Db	501	TyrValIleIlePheHisProGluGlnAsnValGlnLysArgLysArgSerPheGlyAla	520
Qy	1603	GTGGTCAACCGCCACCATGTCCAAAGTTCCACAGAAAGGCGCACTTCCAGGCCAAT	1662
Db	521	ValValGlnAlaAlaThrValSerThrArgLeuSerGlnLysSerSerAspLysGlnAsn	540
Qy	1663	GGGGAAGCCCAATCAGAG	1680
Db	541	GlyGluSerLysIleGlu	546


```
RESULT 5
A46742
metabotropic glutamate receptor, mGluR6 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46742
R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, J.; Biol. Chem. 268, 11868-11873, 1993
A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor m
A:Reference number: A46742; MUID:93280152; PMID:8389366
A:Accession: A46742
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-871 <NA>
A:Cross-references: UNIPROT:P35349; GB:D13963; NID:g391856; PIDN:BA03066.1; PID:g391857
A:Experimental source: retina
A>Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBI:P:133250)
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; transmembrane protein

Alignment Scores:
Pred. No.: 3,096-124 Length: 871
Score: 2026.50 Matches: 379
Percent Similarity: 74.24% Conservative: 62
Best Local Similarity: 63.80% Mismatches: 97
Query Match: 61.35% Indels: 56
DB: 2 Gaps: 2

US-10-828-332-6 (1-1755) x A46742 (1-871)
QY 3 GCCAGGGTATCATCTTTGCCAAGCAGGATGACATCA----- 42
DB 267 AlaArgGlyIleIleIlePheAlaAsnGluAspAep-IleArgArgValLeuGluAlaTh 286
QY 42 ----- 42
DB 286 rArgGlnAlaAsnLeuThrGlyHisPheLeuTrpValGlySerAspSerTrpGlySerLy 306
QY 42 ----- 42
DB 306 sIleSerProIleLeuAsnLeuGluGluAlaValGlyAlaIleThrIleLeuProLy 326
QY 43 -----GGTTCGACCGATCTCTCCAGCGCAGCGCGGACACACAG 86
DB 336 sArgAlaSerIleAspGlyPheAspGlnTrpPheMetThrArgSerLeuGluAsnAsnAr 346
QY 87 GCGCAACATCTGTTTGGCGAGTTCTGGGAGACAACTTCCATTGCCAAGTTGAGCGCGCA 146
DB 346 gArgAsnIleTrpPheAlaGluPheTrpGluAsnPheAsnCyAlaValLeuThrSerSe 366
QY 147 CCGCTCAAGAGGAGAACCCATCAAGAGTGCACCAACCGAGAGCGATCGGGCAGGA 206
DB 366 rGlyGlyGlnSerAspAspSerThrArgLysCysThrGlyGluGluArgIleGlyGlnAs 386
QY 207 CTCGGCTATGACAGGAGGAGGAGTCTGATTCAGCTGATTCAGCTGATTCAGCTGATGG 266
DB 386 pSerAlaTrpGluGlnGluGlyLysValGlnPheValIleAspAlaValTrpAlaIleAl 406
QY 267 CCACCGCTGACCGCATCGACCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 326
DB 406 aHisAlaLeuHisSerMetHisGlnAlaLeuCysProGlyHisThrGlyLeuCyProAl 426
QY 327 CATGACCCCGTGGATGGACCCAGCTGCTTAAGTACATCAGGAACGCTCAACTCTCAGG 386
DB 426 aMetGluProThrAspGlyArgThrLeuLeuHisIleArgAlaValArgPheAsnGln 446
QY 387 CATTCGGGGGACCTGTAACTTCAATCAGAACCGAGACCGACCGGGCGCTACGACAT 446
DB 446 ySerAlaGlyThrProValMetPheAsnGluAsnGlyAspAlaProGlyArgGlyAspIl 466
QY 447 CTACAGGTACCAACTCGCGCAATGGCTCGCGCCGAG-----TACAGGTGTCATCGGCTC 497
DB 497 -----TACAGGTGTCATCGGCTC 497
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DB 466 ePheGlnTrpGlnAlaThrAsnGlySerAlaSerSerGlyGlyTrpGlnAlaValGlyGl 486
QY 498 GTGGACAGACACCTGTCACCTCAGATAGAGCGATGCGAGTGGCCAGGAGTGCCAGCA 557
DB 486 nTrpAlaGluAlaLeuArgLeuAspMetGluValLeuArgTrpSerGlyAspProHisGl 506
QY 558 GCTGCCCGCGCTCCATCTGTCAGTCTGCCCTCCAGCGCGGGAGCGAAAGAGACTGTGA 617
DB 506 uValProProSerGlnCysSerLeuProCyAsGlyProGlyGluArgLysMetValLy 526
QY 618 GGGCATCGTGTCTGTCGTCGAGCCCTGCAGCCCTGCACCGGGTACACAGTACCAAGTGGACCG 677
DB 526 sGlyValProCysCysTrpHisCysGluAlaCysAspGlyTrpArgPheGlnValAspGl 546
QY 678 CTACACCTGTAAAGACCTGCCCTACGACATGCGGCCCCACAGAGACCGACGACTGCCA 737
DB 546 uPheThrCysGluAlaCysProGlyAspMetArgProThrProAsnHisThrGlyCysAr 566
QY 738 GCCCATCCCATCTCAAGTTGGAGTGGGACTCCGCCGTGGCGCTGCTGCTGCTGCTTCTCT 797
DB 566 gProThrProValValArgLeuThrTrpSerSerProTrpAlaAlaLeuProLeuLeuLe 586
QY 798 GCGCGTGGTGGCATCCGCCACGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 857
DB 586 uAlaValLeuGlyIleMetAlaThrThrIleMetAlaThrPheMetArgHisAsnAs 606
QY 858 TACCCCATCGTCAAGGCGCTCGGGCGGAACTGAGCTAGCTGCTGCTGCTGCTGCTGCTGCT 917
DB 606 pThrProIleValArgAlaSerGlyArgGluLeuSerTrpValLeuLeuThrGlyIlePh 626
QY 918 TCTGTGCTAGCCACTACCTTCTCATGATCGCAGAGCGCGACCTGGGGACCTGCTGCTGCT 977
DB 626 eLeuIleTrpAlaIleThrPheLeuMetValAlaGluProCysAlaAlaIleCysAlaAl 646
QY 978 CCGCGCATCTTCTCAGGCTCGGCATGAGCATCAGCTAGCTGCTGCTGCTGCTGCTGCTGCTG 1037
DB 646 aArgArgLeuLeuLeuGlyLeuGlyThrThrLeuSerTrpSerAlaLeuLeuThrLyTh 666
QY 1038 CAACCGCATTTACCGCATCTTTGAGCAGGCGCAACGCTCGCTGCTGCTGCTGCTGCTGCTGCT 1097
DB 666 rAsnArgIleTrpArgIlePheGluGlnGlyLysArgSerValThrProProProPheIl 686
QY 1098 CAGCGCGCTCGCAGCTGCGCATCCTCATCTCTCATCTCTCTGCTGCTGCTGCTGCTGCTGCT 1157
DB 686 eSerProThrSerGlnLeuValIleThrPheGlyLeuThrSerLeuGlnValValGlyVa 706
QY 1158 CTGCGTGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1217
DB 706 lIleAlaTrpLeuGlyAlaGlnProProHisSerValIleAspTrpGluGluGlnArgTh 726
QY 1218 ACTTGACCCCGCTTTCGAGGGCGTCTCAAGTGGAGCATCTCGGACCTGCTGCTGCTGCTGCT 1277
DB 726 rValAspProGluGlnAlaArgGlyValLeuLysCysAspMetSerAspLeuSerLeuIl 746
QY 1278 CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1337
DB 746 eGlyCysLeuGlyTrpSerLeuLeuLeuMetValThrCysThrValTrpAlaIleLysAl 766
QY 1338 CCGAGGGCTGCCGAGACCTTCAAGAGGCGCAACCCATCGGCTGCTGCTGCTGCTGCTGCTGCT 1397
DB 766 aArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPheThrMetTrpThrTh 786
QY 1398 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
DB 786 rCysIleIleTrpLeuAlaPheValProIlePhePheGlyThrAlaGlnSerAlaGluLy 806
QY 1458 GCTGTATATCCAGAACCAACACTGAGCGTCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1517
DB 806 sIleTrpIleGlnThrThrThrLeuThrValSerLeuSerLeuSerAlaSerValSerLe 826
QY 1518 GGGGATGCTTACATGCCCAAGTCTCATCATCTCTTCCACCGGAGCAGACGTGCC 1577
DB 826 uGlyWetLeuTrpValProLyThrTrpValIleLeuPheHisProGluGlnAsnValGl 846
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QY 1578 CAAGCGCAAGCGCAGTCTCAAGCCGTGTCTACCGCGCCG 1617
 Db 846 nlysrArglysrArgSerLeuylsYsrThrSerThrMetAla 859

RESULT 6
 JH0561
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 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: JH0561
 R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 Neuron 8, 169-179, 1992
 A:Title: A family of metabotropic glutamate receptors.
 A:Reference number: JH0561; MUID:92110002; PMID:1309649
 A:Accession: JH0561
 A:Molecule type: mRNA
 A:Residues: 1-872 <TAN>
 A:Cross-references: UNIPROT:P31421
 A:Experimental source: brain
 C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m
 C:Superfamily: metabotropic glutamate receptor 4
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
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 F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>
 F:568-590/Domain: transmembrane #status predicted <TRI>
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Alignment Scores:
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 Query Match: 35.47% Indels: 41
 Db: 2 Gaps: 10

US-10-828-332-6 (1-1755) x JH0561 (1-872)

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 Db 335 AppProTyrPheAsnSerArgAsnProTyrPheArgGluPheTyrGluArgPheHis 354
 QY 130 TGCAGTTG-----AGCGCCACGCGCTCAAGAGGAGGCCACATCAAG 174
 Db 355 CysSerPheArgGlnArgAspCysAlaAlaHisSerLeuArgAla----- 369
 QY 175 AGTGCACCAACGAGAGCGCATCGGCGAGGACTCGGCTATGACGAGGAGGGAGGTG 234
 Db 370 -----ValProPheGluGlnSerLysIle 378
 QY 235 CAGTTGCGTATTGACGTGTAGCGCATGGCGCGCTCGACCGCATGACCGTGAC 294
 Db 379 MetPheValValAsnAlaValTyrAlaMetAlaHisAlaLeuHisAsnMethisArgAla 398
 QY 295 GTGTGTCCCGCGCGTAGGACTCTGCTCGCATGGACCCCGTGGATGGCCACCGCTG 354
 Db 399 LeuCysProAsnThrThrHisLeuLeuCysAspAlaMetArgProValAsnGlyArgLeu 418
 QY 355 CTTAG-----TACATCGGAGCGTCACTCTCA-----GGCATTCGGGG 396
 Db 419 TyrLysAspPheValLeuAsnValLysPheAspAlaProPheArgProAlaAspThrAsp 438

QY 397 AACCTCTGTAACCTTCAATGAGAACGAGACGACCGCGGCGCTACGACATCTACCGATAC 456
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 QY 511 CTGACCTCTCAGAAATAGAGCGGATGAGTGG-----CCAGGAGGAGCGGACGAGCTGCG 564
 Db 478 LeuThrLeuAspThrSerPheIleProTyrPheAlaSerProSerAlaGly---ProLeuPro 496
 QY 565 CGCTCTCATCTGACAGTCTCGCTCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 624
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 QY 805 GTGGGCGATCGCGCGCGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
 Db 577 LeuGlyAlaLeuAlaThrLeuPheValLeuGlyValPheValArgHisAlaThrPro 596
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 QY 1105 GCCTCGCAGCTGCGCATCACCTTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1164
 Db 677 AlaSerGlnValAlaIleCysLeuAlaLeuIleSerGlyGlnLeuLeuIleValAlaAla 696
 QY 1165 TGT 1224
 Db 697 TrpLeuValValGluAlaProGlyThr-----GlyLysGluThrAlaPro 711
 QY 1225 CCGCGTTTTCAGGCGGCTGCTCAAGTGCAGCATCTCGACCTCTGCTCTCTCTCTCTCTCT 1284
 Db 712 GluArgArgGluValValThrLeuArgCysAsnHisArgAspAlaSerMetLeuGlySer 731
 QY 1285 CTGGGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1344
 Db 732 LeuAlaTyrAsnValLeuLeuIleAlaLeuCysThrLeuTyrAlaPheLysThrArgLys 751
 QY 1345 GTGCGCGAGCTTCAACGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 1404
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 QY 1405 GTCTGGCTGGCTTCTATCCCATCTTTTGTGCGACCTCACAGTCCAGCGGAGCGGAGCTG 1464
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QY 1375 ATCGCTTCACCATGTATACACCACTGCAATTCCTGGCTGGCTTCATCCCATCTTTT 1434
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QY 1435 GGCACCTCAGTCAAGCCGACAAAGCTGTACATCCAGAACACACACTGACGGTCTCCGTG 1494
Db 791 ValThrSerSerAsp-----TyrArgValGlnThrThrThrMetCysIleSerVal 807
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Db 808 SerLeuSerGlyPheValValLeuGlyCysLeuPheAlaProLysValHisIleValLeu 827
QY 1555 TTCACACCGGAGCAGAAAGTGCACCAAGCGCAAGCGCAGTCTCAAAGCGGTGGTCAACGCC 1614
Db 828 PheGlnProGlnLysAsn-----ValValThrHis 837
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Db 838 ArgLeuHisLeuAsnArgPheSerValSerGly 848
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JC2132
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C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2132
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: JC2131; MUID:94197696; PMID:7908515
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Query Match: 34.00% Indels: 29
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US-10-828-332-6 (1-1755) x JC2132 (1-1180)
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QY 67 CGCAGCTGGACAAACACAGCGGCAACATCTGGTTTGGCGAGTTCGGAGGACACATTC 126
Db 344 LeuArgProGluThrAsnHisArgAsnProIlePheGlnGluPheIleIleIleIleIle 363
QY 127 CATTCGAGTTGAGCGGCCCGCCAGCGCTCAAGAGGGAAGCCACATCAAGAGTGCACCAAC 186
Db 364 GlnCysArgLeuGluGlyPheProGlnGluAsnSerLysTyrAsnLysThrCysAsnSer 383
QY 187 CGAGAGCGCATCGGGCAGGACTCGGCCCTATGAGCAGGAGGGGAGGTCAGTTCGTGATT 246

Db 384 -----SerLeuThrLeuLysThrHisHisValGlnAspSerLysMetGlyPheValIle 401
QY 247 GAGCTGTGTAGCGCATGAGCGCCAGCGCTGACCGCATGACCGTGTGTGTCTCCCGGC 306
Db 402 AsnAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 421
QY 307 CGCGTAGGACTCTGCCCTCGCATGGACCCCGTGGATGGACCCAGCTGCTTAAGTACATC 366
Db 422 TyrAlaGlyLeuCysAspAlaMetLysProIleAspGlyArgLysLeuLeuGluSerLeu 441
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Db 442 MetLysThrAsnPheThrGlyValSerGlyAspThrIleLeuPheAspGluAsnGlyAsp 461
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QY 604 AAGAAGACTGTGAAGGCG---ATGGCTTGTCTGGCACTGCGAGCCCTGCGCGGCTAC 660
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QY 1021 GCCCTGTGACCAAGACCAACCGCATTTACCGCATTTTTCGAGCAGGGCAACCGTCCGTC 1080
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 17, 2005, 18:28:23 ; Search time 54 Seconds
(without alignments)
4852.189 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 3303

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3050.5	92.4	604	4	US-09-820-809-13 Sequence 13, Appl
2	3050.5	92.4	912	5	PCT-US91-09422-19 Sequence 19, Appl
3	3004.5	91.0	912	3	US-08-617-785-2 Sequence 2, Appl
4	3004.5	91.0	912	3	US-09-641-318-2 Sequence 2, Appl
5	3004.5	91.0	912	4	US-09-817-464-2 Sequence 2, Appl
6	2370	71.8	908	3	US-08-855-146-2 Sequence 2, Appl
7	2328	70.5	908	3	US-08-823-110-1 Sequence 1, Appl
8	2328	70.5	908	3	US-08-604-298-1 Sequence 1, Appl
9	2219	67.2	915	3	US-08-617-785-12 Sequence 12, Appl
10	2219	67.2	915	4	US-09-817-464-12 Sequence 12, Appl
11	2210	66.9	915	1	US-08-453-862-2 Sequence 2, Appl
12	2210	66.9	915	2	US-08-452-734A-2 Sequence 2, Appl

13	2210	66.9	915	3	US-08-176-401B-2 Sequence 2, Appl
14	2210	66.9	915	5	PCT-US94-14989-2 Sequence 2, Appl
15	2191.5	66.3	867	3	US-08-617-785-4 Sequence 4, Appl
16	2191.5	66.3	867	4	US-09-817-464-4 Sequence 4, Appl
17	2191.5	66.3	922	3	US-08-617-785-14 Sequence 14, Appl
18	2191.5	66.3	922	4	US-09-817-464-14 Sequence 14, Appl
19	2054	62.2	877	2	US-08-407-875-2 Sequence 2, Appl
20	2054	62.2	877	3	US-09-277-858-2 Sequence 2, Appl
21	2042	61.8	877	3	US-09-126-280-2 Sequence 2, Appl
22	1861.5	56.4	481	3	US-08-617-785-8 Sequence 8, Appl
23	1861.5	56.4	481	4	US-09-817-464-8 Sequence 8, Appl
24	1172.5	35.5	872	3	US-08-337-797A-2 Sequence 2, Appl
25	1172.5	35.5	872	3	US-09-258-523-2 Sequence 2, Appl
26	1155.5	35.0	879	1	US-08-794-158-2 Sequence 2, Appl
27	1148.5	34.8	879	1	US-08-072-574-6 Sequence 6, Appl
28	1148.5	34.8	879	3	US-08-486-270-6 Sequence 6, Appl
29	1148.5	34.8	879	3	US-08-367-264-6 Sequence 6, Appl
30	1148.5	34.8	879	4	US-09-153-757-6 Sequence 6, Appl
31	1148.5	34.8	879	4	US-09-459-715-6 Sequence 6, Appl
32	1129	34.2	1194	3	US-08-538-526-1 Sequence 1, Appl
33	1124	34.1	1043	4	US-09-695-481-6 Sequence 6, Appl
34	1124	34.0	1056	2	US-08-687-289A-8 Sequence 8, Appl
35	1123	34.0	1056	4	US-09-435-897-8 Sequence 8, Appl
36	1123	34.0	942	4	US-09-695-481-2 Sequence 2, Appl
37	1123	34.0	1180	3	US-08-660-148-2 Sequence 2, Appl
38	1123	34.0	1212	3	US-08-660-148-5 Sequence 5, Appl
39	1123	34.0	1212	4	US-09-695-481-7 Sequence 7, Appl
40	1122	34.0	1199	1	US-08-041-538-2 Sequence 2, Appl
41	1122	34.0	1199	1	US-08-463-642-2 Sequence 2, Appl
42	1122	34.0	1199	1	US-08-455-602-2 Sequence 2, Appl
43	1122	34.0	1199	2	US-08-465-157-2 Sequence 2, Appl
44	1122	34.0	1199	5	PCT-US91-09422-2 Sequence 2, Appl
45	1121.5	34.0	878	4	US-09-826-509-347 Sequence 347, App

ALIGNMENTS

RESULT 1

US-09-820-809-13
; Sequence 13, Application US/09820809
; Patent No. 6608176
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARI, NIRUPA
; TITLE OF INVENTION: TASTE RECEPTOR FOR UMAMI (MONOSODIUM GLUTAMATE) TASTE
; FILE REFERENCE: 70373/275576
; CURRENT APPLICATION NUMBER: US/09/820,809
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,454
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-820-809-13

Alignment Scores:
Pred. No.: 1.48e-239 Length: 604
Score: 3050.50 Matches: 575
Percent Similarity: 98.97% Conservative: 2
Best Local Similarity: 98.63% Mismatches: 5
Query Match: 92.36% Indels: 1
DB: 4 Gaps: 1

US-10-828-332-6 (1-1755) x US-09-820-809-13 (1-604)

Qy 7 GGGGTATCATCTTTGCCAACGAGATGACA---TCAGGGTTCCGACCGATCTTCTCC 63
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Db 22 GlyalalvalthrlleuProlyseArgMetSerValargGlyPheAspArgTyPheSer 41
|||||

Qy 64 AGCCGCAGCTGGGACAAACAGCGGCAACATCTGGTTTCCGAGTCTCTGGAGGACAAC 123
|||||

Db 42 SerArgThrLeuAspAsnAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 61
Qy 124 TTCATTGCAAGTTGAGCGCCACCGCTCAAGAGGGAAGCCACATCAAGAGTGCACC 183
Db 62 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 81
Qy 184 AACCGAGAGCCATCGGCGAGACTCGCCCTATGAGCAGAGGAGGAGGTCAGTTCGTG 243
Db 82 AsnArgGluArgIleGlyGlnAspSerAlaTrpGluGlnGluGlyLysValGlnPheVal 101
Qy 244 ATTGACGCTGTGTACGCCATGGCCACCGCTGCACGCCATCGACCGTGCCTGTGTC 303
Db 102 IleAspAlaValTyAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 121
Qy 304 GCGCGCTAGACTCTGCGCTCGCATGACACCCCGTGGATGGCACCGACTGCTTAAGTAC 363
Db 122 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysTyr 141
Qy 364 ATCAGGACGTCAACTTCTCAGGCAATTCGCGGGAACCTGTAACTTCAATGAGAACGGA 423
Db 142 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 161
Qy 424 GACGACCGCGCGCTACGACATCTACCACTACCACTCGCAATGGCTCGCGCGAGTAC 483
Db 162 AspAlaProGlyArgTyAspIleTyGlnTyGlnLeuArgAsnGlySerAlaGluTyr 181
Qy 484 AAGTCACTGCGCTGTGACAGACACACTGACCTCAGAAATAGACGATGACAGTGC 543
Db 182 LysValIleGlySerTrpThrAspHisLeuArgIleGluArgMetGlnTrpPro 201
Qy 544 GGGAGTGGCCAGCAGTCGCGCTCCATCTGCAGTCTGCGCTCGCCGCGGAGGAGGGA 603
Db 202 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 221
Qy 604 AAGAAGACTGTGAAGGCGATGCTTGTCTGCTGGCACCTCGAGCCCTGCACCGGTTAC 663
Db 222 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyGln 241
Qy 664 TACCAAGTGGACCGCTACACTGTGAAGACCTGCGCCCTACGACATGCGCGCCACAGAGAAC 723
Db 242 TyrGlnValAspArgTyThrCysLysThrCysProTyArgMetArgProThrGluAsn 261
Qy 724 CGCAGACTGCCAGCCATCCCATCTCAAGTTGGAGTGGAGTGGAGTGGCGCGCTG 783
Db 262 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 281
Qy 784 CTGCGCTCTTCTCGCGCTGTGGGCATCGCGCCACGCTGTTCTGTGGTGGTTCACGTTT 843
Db 282 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValValThrPhe 301
Qy 844 GTGCGCTACAGATACCCCATCTCAAGGCTCGCGCGCGGAACTGAGCTAGTGTG 903
Db 302 ValArgTyAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyValLeu 321
Qy 904 CTGGCGGCCTTTCTGTGCTACGCCACTCTCTCATGATCGCAGAGCGAGCTG 963
Db 322 LeuAlaGlyIlePheLeuCysTyAlaThrThrPheLeuMetIleAlaGluProAspLeu 341
Qy 964 GGGACTGTGTGCTCGCGCATCTTCTTAGGGCTCGGCATGAGCATCAGCTACGCGCC 1023
Db 342 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyAlaAla 361
Qy 1024 CTGCTGACACAGACCAACCGCATTTACCGCATCTTTGAGAGGGGAAACCGTGTGCTAGT 1083
Db 362 LeuLeuThrLysThrAsnArgIleTyArgIlePheGluGlnGlyLysArgSerValSer 381
Qy 1084 GCCCGCTTTCTACAGCCGCGCTCGAGCTGGCCATCCTTCTCATCTCTCCCTG 1143
Db 382 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuSerLeu 401
Qy 1144 CAGCTGCTCGGCATCTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1203

Db 402 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 421
Qy 1204 CAGGACCAAGCGACACTTGGACCCCGCTTGGCCAGGCGCTCAAGTGGAGCATCTCG 1263
Db 422 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 441
Qy 1264 GACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
Db 442 AspLeuSerLeuIleCysLeuLeuGlyTySerMetLeuLeuMetValThrCysThrVal 461
Qy 1324 TACGCCATCAAGACCCGAGCGTGGCCGAGACCTTCAACGAGGCGCAAGCCATCGGCTTC 1383
Db 462 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 481
Qy 1384 ACCATGTACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
Db 482 ThrMetTyThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 501
Qy 1444 CAGTCACCGCACAGCTGTATACATCCAGACCAACACACTGAGCGTCTCCGTGAGTCTGAGC 1503
Db 502 GlnSerAlaAspLysLeuTyIleGlnThrThrThrLeuThrValSerValSerLeuSer 521
Qy 1504 GCTTCAGTGTCCCTGGGGATGCTCTATGCGCCAAAGTCTACATCATCTCTTTCACCCG 1563
Db 522 AlaSerValSerLeuGlyMetLeuTyMetProLysValTyIleIleLeuPheHisPro 541
Qy 1564 GAGCAGACGTCGCCAAGCGCAGCGAGTCTCAAGCGGTGTCACCGCGCCACCATG 1623
Db 542 GluGlnAsnValProLysArgLysSerLeuLysAlaValThrAlaAlaThrMet 561
Qy 1624 TCCAACTGTTTCAACAGAGGCGCACTTCAGGCCCCAATGGGAGGCCAAATCAGAGCTG 1683
Db 562 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 581
Qy 1684 TGTGAGAACCTGGAGACCCCGCTGCTACCAACAGACCTAGCTACCTACCTACCAAC 1743
Db 582 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyValThrThrAsn 601
Qy 1744 CATGCCATC 1752
Db 602 HisAlaIle 604

RESULT 2
PCT-US91-09422-19
; Sequence 19. Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481

; FILING DATE: 30-JAN-1991
 ; PRIOR APPLICATION DATA: US 07/626,806
 ; APPLICATION NUMBER: 12-DEC-1990
 ; FILING DATE: 12-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 13952-6PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 912 amino acids
 ; TYPE: AMINO ACIDS
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US91-09422-19

Alignment Scores:
 Pred. No.: 1.75e-239 Length: 912
 Score: 3050.50 Matches: 575
 Percent Similarity: 98.97% Conservative: 2
 Best Local Similarity: 98.63% Mismatches: 5
 Query Match: 92.36% Indels: 1
 DB: 5 Gaps: 1

US-10-828-332-6 (1-1755) x PCT-US91-09422-19 (1-912)

QY	7	GGGGTATCATCTCTTGGCCACAGGATGACA---TCAGGGTTCGACCATCTCTCC	63
DB	330	GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer	349
QY	64	AGCCGACGCTGGACAAACAGGCGCAACATCTGGTTGCCAGTTCGGGAGGACAAAC	123
DB	350	SerArgThrLeuAspAsnAsnArgAsnIleTrrPheAlaGluPheTrrPheAspAsn	369
QY	124	TTCCATTGCAAGTTGAGCGCCACCGCTCAAGAGGGAGGACACATCAAGAAAGTGCACC	183
DB	370	PheHisCysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr	389
QY	184	ACCAGAGCGCATCGGCGAGACTCGGCTATGACGAGGGAGGAGGAGTGCAGTTCGTG	243
DB	390	AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGluGluGlyLysValGlnPheVal	409
QY	244	ATTGACGCTGTGTAGCCATGGCCACGCGCTGCACCGCCATGCACCTGCACCTGTGTC	303
DB	410	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	429
QY	304	GGCCGCTAGGACTCGCCCTCGCATGGACCCCGTGGATGGACCCAGCTGCTTAAGTAC	363
DB	430	GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr	449
QY	364	ATCAGGAGCTCAACTTCAGGCATTCGGGGAACCCCTGTAACTTCATGAGAACGGA	423
DB	450	IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly	469
QY	424	GACGACCGGGCGCTTACGACATCTACAGTACCACTACGCAATGGCTCGGCCCGAGTAC	483
DB	470	AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerIleGluTyr	489
QY	484	AAGGTTCATCGGCTGGGACAGACCATCTGCACCTCAGAAATAGCGGATGCAAGTGGCCA	543
DB	490	LysValIleGlySerTrrPheAspHisLeuHisLeuArgIleGluArgMetGlnTrrPro	509
QY	544	GGAGTGGCCAGCTGGCGGCTCCATCTGCAGTCTGCCCTGCACGCCCGGGAGCGA	603
DB	510	GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg	529
QY	604	AGAAGACTGTCAAGGGCATGCTGTGCTGGCACTGCGACCTGCGACCGGGTACCAG	663
DB	530	LysLysThrValLysGlyMetAlaCysCysTrrPheCysGluProCysThrGlyTyrGln	549

QY	664	TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATCGGGCCACAGAGAC	723
DB	550	TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn	569
QY	724	CGCAGAGCTGCAGCCCATCCCATCTCAAGTTGGAGTGGACTCGCCGCTGGGCGGTG	783
DB	570	ArgThrSerCysGlnProIleValLysLeuGluTrrPheSerProTrrPheVal	589
QY	784	CTGCCCTTCTTCCTGGCGGTGGCATCGCCGCGGACGCTTCTCGTGGTGTTCAGTTT	843
DB	590	LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValValThrPhe	609
QY	844	GTGGCTACACAGATACCCCATCTCAAGGCTCGGGCGGGAAGTACGACTACGCTG	903
DB	610	ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu	629
QY	904	CTGGCGGCGATCTTCTGTGTACGCCACTACTCTTCATCATCGCAGAGCGGACCTG	963
DB	630	LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu	649
QY	964	GGGACCTTCTTCCTCCCGCATCTTCTAGGGCTCGGCATGAGCATCAGCTACCGGCG	1023
DB	650	GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla	669
QY	1024	CTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGACGAGCGGCAACGCTCGCTC	1083
DB	670	LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer	689
QY	1084	GCCCGCGTTTCATCAGCCCGCGCTCGCAGCTGGGCATCACCTTCATCTCATCTCCCTG	1143
DB	690	AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu	709
QY	1144	CAGTGTCTCGGCATCTCGCTGTGGTTCGTGGTGGACCCCTCCCATCTCGTGTGGACTTC	1203
DB	710	GlnLeuLeuGlyIleCysValTrrPheValValAspProSerHisSerValValAspPhe	729
QY	1204	CAGACCAACCGACACTTGACCCCGCTTTCGACGGGCGGTGCTCAAGTGCACATCTCG	1263
DB	730	GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer	749
QY	1264	GACCTGTCCCTCATCTCGCTGTGGGTACAGCATGCTGCTGATGGTCACTGCTACTGTG	1323
DB	750	AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal	769
QY	1324	TACGCATCAAGACCCGAGCGCTGCCGAGACCTTCAACAGAGCGCAAGCCCATCGGCTTC	1383
DB	770	TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe	789
QY	1384	ACCATGTACACCATCTGCATTTGCTGGCTGGCTTCATCCCATCTTTTGGCACCTCA	1443
DB	790	ThrMetTyrThrThrCysIleValTrrPheAlaPheIleProIlePhePheGlyThrSer	809
QY	1444	CAGTCAGCGGACAGCTGTACATCCAGAACACACACTGACGCTCTCGTGTAGTCTGAGC	1503
DB	810	GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer	829
QY	1504	GCTTCAGTGTCTTCGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCACCGG	1563
DB	830	AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro	849
QY	1564	GAGCAGAACTGGCCAGCGGACGAGTCTCAAGCGGTGGTTCACCGCGCCACCATG	1623
DB	850	GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet	869
QY	1624	TCCAAACAGTTTCACAGAGCGAACTTCAGGCCCAATGGGAAGCAAAATCACAGCTG	1683
DB	870	SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu	889
QY	1684	TGTGAGAACTTCGAGACCCCGCTGCTGCTACCAAAACAGACTAGTCACTCACCTAC	1743
DB	890	CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn	909
QY	1744	CATGCCATC	1752

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Db      910 HisAlaIle 912
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RESULT 3
US-08-617-785-2
; Sequence 2, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-2

Alignment Scores:
Pred. No.:          9,638-236      Length:          912
Score:             3004.50         Matches:        564
Percent Similarity: 97.77%         Conservative:   6
Best Local Similarity: 96.74%      Mismatches:    12
Query Match:       90.96%          Indels:         1
Db:                 3              Gaps:           1

US-10-828-332-6 (1-1755) x US-08-617-785-2 (1-912)
QY      7 GGGGTATCATCTTTGCCACGAGGATGACA---TCAGGTTTCGACCGATCTCTCC 63
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Db      330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
|||
QY      64 AGCCGACGCTGGACAAACAGCGGCAACATCTGGTTTGGCGAGTTCTGGAGGACAAAC 123
|||
Db      350 SerArgThrLeuAspAsnArgAsnIleTTPheAlaGluPheTrpGluAspAsn 369
|||
QY      124 TTCCATTGCAAGTTGAGCGGCCCGCTCAAGAGGGAGCCACATCAAGAGTGCACC 183
|||
Db      370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysCysThr 389
|||
QY      184 AACCGAGAGCGCATCGGCGAGGACTCGGCTATGAGCAGGAGGGAGAGTGCAGTTCGTG 243
|||
Db      390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
|||
QY      244 ATTGACGCTGTGTAGCCATGGCCACGCGCTGACGCGCATCGACCGCTGTGTCTCC 303
|||
Db      410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
|||
QY      304 GCGCCGTTAGAGTCTGCGCTCGCATGGACCCCGTGGATGGACCCACCTGTTAAGTAC 363
|||
Db      430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
|||
QY      364 ATCAGGAAGCTCAACTCTCAGGCAATCGGGGAACCTGTAACTTCAATGAGAACGGA 423
|||
Db      450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGlnAsnGly 469
|||
QY      424 GACGACCGGGCGCTACGACATCTACCACTACCACTGCGCAATGGCTCGGCCGAGTAC 483
|||
Db      470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
|||

484 AAGTTCATCGCTCGTGACAGACACCTGCACCTCAGAAATAGAGCGGATCGAGTGGCCA 543
|||
Db      490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 509
|||
QY      544 GGGAGTGGCCAGCAGCTGCCCGCTCCATCTGCAGTCTGCCCTGCCAGCCCGGGAGCGA 603
|||
Db      510 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
|||
QY      604 AAGAAGACTGTGAAGGCGATGGCTTGTCTGGCACTGGCAGCCCTGCACCGGCTACCAG 663
|||
Db      530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
|||
QY      664 TACCAGTGGACCGCTACACTGTAAAGACTGCCCTACGACATGCGCGCCACACAGAGAAC 723
|||
Db      550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
|||
QY      724 CGCACGAGCTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGCCGTG 783
|||
Db      570 ArgThrGlyCysArgProIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
|||
QY      784 CTGCCCTCTCTCTGGCGGTGGTGGCATGCCCGCCAGCGCTGTTCGTGGTGGTTCACGTTT 843
|||
Db      590 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValIleThrPhe 609
|||
QY      844 GTGCGCTACAACGATACCCCATCGTCAAGCGCTCGCGCGGGGAACTGAGCTACGTGCTG 903
|||
Db      610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
|||
QY      904 CTGCGGGGCTCTTTCTGTGCTACGCCACTACCTCTCTCATGATCGCAGAGCCGAGCTG 963
|||
Db      630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
|||
QY      964 GGGACCTGTCCTCCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGTACGCGGCC 1023
|||
Db      650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
|||
QY      1024 CTGCTGACCAAGCAACCGCATTTACCGCATCTTTTCAGCAGGCGGCAACCGTCCGTCAGT 1083
|||
Db      670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
|||
QY      1084 GCGCGCGTTTCATCAGCCCGCGCTCGCAGCTGCCCATCACCTTCCTCATCTCCTCGCTG 1143
|||
Db      690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
|||
QY      1144 CAGCTGCTCGGCATCTCGGTGTGGTTCGTGGTGAACCCCTCCCACTCGGTGGTGGACTTC 1203
|||
Db      710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
|||
QY      1204 CAGGACCAACGCGACCTTGACCCCGCTTTGCCAGGCGGTGCTCAAGTGCAGATCTCG 1263
|||
Db      730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
|||
QY      1264 GACTGTCTCTCATCTCGCTGCTGGGTACAGCATGCTGTGATGTGTGTCACGTGTCTGTG 1323
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Db      750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
|||
QY      1324 TAGCCCATCAAGACCCGAGCGGTGCCGAGACCTTCAACGAGGCGCAAGCCCATCGGCTTC 1383
|||
Db      770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
|||
QY      1384 ACCATGTACACCACTCATCTGTGCTGGCTGCTTCATCCCATCTTTTGGCACCTCA 1443
|||
Db      790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 809
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QY      1444 CAGTCAGCCGACAGCTGTACATCCAGACCAACACACTGACGCGTCTCGTGAGTCTGAGC 1503
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Db      810 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 829
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QY      1504 GCTTCAGTGTCTCTGGGGAGTCTTACATGCCCAAGCTTACATCATCTCTTCCACCG 1563
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Db      830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
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QY 1564 GAGCAGACGTCGCCAAGCGCAGCGAGCTCTCAAGCGCTGGTCAACCGCGCCAGCATG 1623
Db |||||
850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 869
QY 1624 TCAACAAGTTACACAGAGGCGCACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG 1683
Db |||||
870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
QY 1684 TGTGAGAACTGGAGACCCAGCGCTGGCTACCAACACAGACCTACCTACCAAC 1743
Db |||||
890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
QY 1744 CATGCCATC 1752
Db |||||
910 HisAlaIle 912

RESULT 4

US-09-641-318-2
; Sequence 2, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; WU, SU
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; AND RELATED NUCLEIC ACID COMPOUNDS

; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: ELI LILLY AND COMPANY
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: INDIANA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 46285

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,318
; FILING DATE: 18-Aug-2000

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,178A
; FILING DATE: 12-MAR-1997
; ATTORNEY/AGENT INFORMATION:

; NAME: GAYLO, PAUL J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10579
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEX: (317) 276-3861

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-641-318-2

Alignment Scores:
Pred. No.: 9.63e-236 Length: 912
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 90.96% Indels: 1
DB: 3 Gaps: 1

US-10-828-332-6 (1-1755) x US-09-641-318-2 (1-912)

QY 7 GGGGTATCATCATCTTTGCCAGGAGGATGACA---TCAGGGTTGACCGATCTCTCC 63
Db |||||
330 GlyAlaValThrIleLeuProLysArgMetSerValArgLysPheAspArgTyrPheSer 349

QY 64 AGCCGACGCTGGACAAACAAAGCGCAACATCTGTTTGGAGTCTTGGAGGACAAC 123
Db |||||
350 SerArgThrLeuAspAsnAsnArgAsnIleTTPheAlaGluPheTrpGluAspAsn 369
QY 124 TTCCATTCCAGTTGAGCGCCGACCGCTCAAGAGGGAAGCCACATCAAGAGTGCCAC 183
Db |||||
370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysLysCysThr 389
QY 184 AACCCAGAGCGCATCGGCGAGACTCGGCTTATGAGCAGAGGAGGAAAGTGCAGTTCTGTG 243
Db |||||
390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyValGlnPheVal 409
QY 244 ATTGACGCTGTGTACGCCATGCGCGCTGCAGCCATGCACCTGCACCTGTGTCTCC 303
Db |||||
410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
QY 304 GCGCGCTAGGACTCTGCGCTCGCATGGACCCCGTGGATGGCACCCAGCTGCTTAAGTAC 363
Db |||||
430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
QY 364 ATCAGGAACGTCAACTTCTCAGGCAATCGGGGAAACCTGTAACTTCAATGAGAACGA 423
Db |||||
450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
QY 424 GAGCACCGCGCGCTACGACATCTACAGTACCACTGCGCAATGGCTCGGCGCGAGTAC 483
Db |||||
470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
QY 484 AGGTCTCATCGCTCGTGACAGACACCTGCACCTCAGATAGAGGAGGATGACAGTGGCCA 543
Db |||||
490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 509
QY 544 GGGAGTGGCAGCAGCTGCGCGCTCATCTGACGTCTGCCCTGCGAGCCGCGGAGCGA 603
Db |||||
510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
QY 604 AAGAAGCTGTGAAGGGCATGCTTGTGCTGGCACTCGAGCCCTGCACCCGGTACCCAG 663
Db |||||
530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCCCTAGACATGGGCCCAAGAC 723
Db |||||
550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
QY 724 GCGCAGCTGCGCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGCGGGCCGTG 783
Db |||||
570 ArgThrGlyCysArgProIleIleLysLeuGluTrpGlySerProThrAlaVal 589
QY 784 CTGCCCCCTTCTCTGCGCGTGGTGGCATCGCCGACGCTGTTCGTGGTGTCAAGTTT 843
Db |||||
590 LeuProLeuPheLeuAlaValGlyIleAlaIleThrLeuPheValIleThrPhe 609
QY 844 GTGCGCTACACGATACCCCATCGTCAAGGCTCGGCGCGGAACTGAGCTACGTCTG 903
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610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
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630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
QY 964 GGGACCTGTCTCGCTCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGCTACCGGCC 1023
Db |||||
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QY 1024 CTGCTGACACAGACCAACCGGATTTACCGCATCTTTGAGCAGGGGAAACCGTGGTCACT 1083
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670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
QY 1084 GCCCGCGCTTTCATCAGCCCGCGCTCGCAGCTGGCCATCACCTTCACTCTATCTCCCTG 1143
Db |||||
690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709

1144 CAGCTGCTCGGCATCTGCTGGTGGTTCGTGGTGGACCCCTCCACTCGGTGGTGGACTTC 1203
|||||
Db 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
1204 CAGGACCAACGACACTTGGACCCCGCTTTGCGAGGGCGGTCTCAAGTGGACATCTCG 1263
|||||
Db 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
1264 GACCTGCTCCCTCATCTGCTGCTGGCTACAGCATGCTGCTGATGCTGCTGCTGCTGCTG 1323
|||||
Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
1324 TACGCCATCAAGACCCGAGGGCTGCCGAGACCTTCAACGAGGCCCAACCCCATCGGCTTC 1383
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Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
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Db 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 809
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Db 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 829
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1564 GAGCAGAACGTCGCCAAGCGCAGTCTCAAGCGGTGTCACCGCGCCCAACCATG 1623
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Db 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 869
1624 TCCACAGTTCACACAGAGGCACTTCAGGCCAATGGGAGCCCAATCAGAGCTG 1683
|||||
Db 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
1684 TGTGAGAACCTGGAGACCCCGCTGCTACCAACAGACTCAGTCACTCAGTCACTACACCAAC 1743
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Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrValThrTyrThrAsn 909
1744 CATGCCATC 1752
|||||
Db 910 HisAlaIle 912

RESULT 5

US-09-817-464-2
; Sequence 2, Application US/09817464
; Patent No. 6515107
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttnier, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/09/817,464
; CURRENT FILING DATE: 2001-03-26
; EARLIER APPLICATION NUMBER: US/08/617,785
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-464-2

Alignment Scores:
Pred. No.: 9,63e-236 Length: 912
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 90.96% Indels: 1
DB: 4 Gaps: 1
US-10-828-332-6 (1-1755) x US-09-817-464-2 (1-912)
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Db 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
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Qy 64 AGCCGACGCTGGACAAACAGCGCAACATCTGCTTTCGCGAGTCTCGGAGGACAAAC 123
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Db 350 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 369
|||
Qy 124 TTCCATTGCAAGTTGAGCCCGCCAGCGCTCAAGAGGGAAGCCACATCAAGAAAGTGCAAC 183
|||
Db 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysLysCysThr 389
|||
Qy 184 AACGAGAGCGCATCGGCGAGGACTCGGCTTATGAGCAGAGGAGGGAAGTGCAGTCTGTG 243
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Db 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
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Qy 244 ATTGACGCTGTGTACGCATGGGCGCACGCTGCACGCCCATGCACCGTACCTGTGTCCC 303
|||
Db 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
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Qy 304 GGCCGCTAGGACTCTCTCCCTCGCATGGACCCCGTGGATGGCACCCAGCTGCTTTAAGTAC 363
|||
Db 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysLysTyr 449
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Qy 364 ATCAGGAACGCTAACTTCTCAGGCATTCGCGGGAACCCCTGTAACTTCAATGAGAACCGGA 423
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Db 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
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Qy 424 GAGCAGCGGGCGCTACGACATCTACAGTACCACTGCGCAATGCTGCGCGAGTAC 483
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Qy 484 AAGTCTATCGGCTCGTGGACAGACCATCTGCACCTCAGAATAGAGCGGATGCAGTGGCCA 543
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Db 490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 509
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Qy 544 GGGAGTGGCGAGCTGCGCGCTCCATCTGCGAGTCTGCGCTGCGCGCGGAGGCGGA 603
|||
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Qy 604 AAGAAGACTGTGAAGGCGCATGGCTTGTCTGGGCACTGCGAGCCCTGCACCGGTACCCAG 663
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Db 530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
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Qy 664 TACCAAGTGGACCGCTACACTGTGAAGACCTGCCCCCTACGACATGCGCGCCCAAGAGAAC 723
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Qy 724 CGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGAGTGGAGTGGAGTGGAGTGGAGTGG 783
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Db 570 ArgThrGlyCysArgProIleProIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
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Qy 784 CTGCCCCCTCTTCCTGGCGGTGGGATCGCCCGCACCGCTGTTGTTGGTGGTTCACGTTT 843
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DB 670 LeuLeuThrLysThrAsnArgileTyrArgilePheGluGlnGlyArgSerValSer 689
QY 1084 GCCCGCGTTTCATCAGCGCGCGCTCGCAGCTGGCATCACCTTCATCTCATCTCCCTG 1143
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QY 1144 CAGCTGCTCGGCATCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1203
DB 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
QY 1204 CAGGACCAACGACACTTACCGCGCTTTCAGCGGGGCTCTCAAGTCGACATCTCG 1263
DB 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
QY 1264 GACCTGCTCCCTCATCTGCTGCTGGGCTACAGCATGCTGCTGCTGCTGCTGCTGCTG 1323
DB 750 AspleuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
QY 1324 TAGCGCATCAAGACCGAGCGCTGCGGAGACTTCAACGAGGCGCAAGCCCATCGGCTTC 1383
DB 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
QY 1384 ACCATGTATACACCATCTGATGTTGCTGGCTTTCATCCCATCTTTTGGCACCTCA 1443
DB 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 809
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DB 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 829
QY 1504 GCTTCAGTGTCTCGGGATGCTTACATGCCCAAGTCTACATCATCTCTTCCACCGG 1563
DB 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro 849
QY 1564 GAGCAGACGTGCCCCAAGCGGAGCGGCTCTCAAGCGGCTGCTACCGCGCCACCATG 1623
DB 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 869
QY 1624 TCCAAAGATTCCACACAGAGGCAACTTTCAGCGCCCAATGGGAGGCAAAATCACAGCTG 1683
DB 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
QY 1684 TGTGAGAACCTGGAGACCCCGCTGCTACCAACAGACCTACCTCACCTACACCAAC 1743
DB 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 909
QY 1744 CATGCCATC 1752
DB 910 HisAlaIle 912

RESULT 6

US-08-855-146-2

; Sequence 2, Application US/08855146

; Patent No. 6221609

; GENERAL INFORMATION:

; APPLICANT: Belagaje, Rama M.

; APPLICANT: Wu, Su

; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN

; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Eli Lilly and Company

; STREET: Lilly Corporate Center/Patent Department

; CITY: Indianapolis

; STATE: IN

; COUNTRY: USA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/855,146

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/021,243

; FILING DATE: 07-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Webster, Thomas D.

; REGISTRATION NUMBER: 39,872

; REFERENCE/DOCKET NUMBER: X-10836

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (317) 276-63334

; TELEFAX: (317) 276-2764

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 908 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-855-146-2

Alignment Scores:

Pred. No.:	3,69e-184	Length:	908
Score:	2370.00	Matches:	437
Percent Similarity:	84.91%	Conservative:	58
Best Local Similarity:	74.96%	Mismatches:	86
Query Match:	71.75%	Indels:	2
DB:	3	Gaps:	2

US-10-828-332-6 (1-1755) x US-08-855-146-2 (1-908)

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DB 327 GlyAlaValThrIleLeuProLysArgAlaSerIleAspGlyPheAspArgTyrPheArg 346
QY 64 AGCGCGACGCTGGGCAACAACAGCGGCAACATCTGTTTGGCGAGTCTCTGGGAGACAAC 123
DB 347 SerArgThrLeuAlaAsnAsnArgAsnValTrpPheAlaGluPheTrpGluGluAsn 366
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DB 367 PheGlyCysLysLeuGlySerHisGly---LysArgAsnSerHisIleLysLysCysThr 385
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QY 304 GCGCGCTAGGACTCTGCTTCCCTCGCATGACCCCGTGGATGGCACCCAGCTCTTAAGTAC 363
DB 426 GlyTyrIleGlyLeuCysProArgMetSerThrIleAspGlyLysLeuLeuGlyTyr 445
QY 364 ATCAGGAACGTCAACTTCTCAGGCATTCGCGGGGAACCTGTAACTTCAATGAGAACGGA 423
DB 446 IleArgAlaValAsnPheAsnGlySerAlaGlyThrProValThrPheAsnGluAsnGly 465
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DB 466 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnIleThrAsnLysSerThrGluTyr 485
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DB 486 LysValIleGlyHisTrpThrAsnGlnLeuHisLysValGluAspMetGlnTrpAla 505

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Db 546 TyrGlnValAspGluLeuSerCysGluLeuCysProLeuAspGlnArgProAsnMetAsn 565
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QY 1024 CTGTGTACACAGCAACCGCATTTACCGCATCTTTTGAGAGGGCAACGGTCTGGTCAGT 1083
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Db 786 ThrMetTyrThrThrCysIleIleThrLeuAlaPheIleProIlePheGlyThrAla 805
QY 1444 CAGTCAGCGGACAGCTGTACATCAGACACACACCTGAGCGGTCTCGTGGTCTGAGTCTGAGC 1503
Db 806 GlnSerAlaGluLysMetTyrIleGlnThrThrThrLeuThrValSerMetSerLeuSer 825
QY 1504 GCTTCAGTGTCTCGGGATGCTGTACATGCGCCAAAGTCTACATCATCTCTTCCACCGC 1563
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QY 1564 GAGCAGAACGTGCCCCAAGCGCAGTCTCAAAGCGGTGGTCAACCGCGCCCGCCACCATG 1623
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QY 1624 TCCAACAAGTTCCACAGAAAGGGCACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG 1683
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QY 1684 TGTGAGAACTGGAGACCCCGAGCTGGCTACCAACAGAGACCTTACGTCACCTACACCAAC 1743
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RESULT 7
US-08-823-110-1
; Sequence 1, Application US/08823110
; Patent No. 6077675
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,110
; FILING DATE: March 24, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,298
; FILING DATE: February 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-823-110-1
Alignment Scores:
Pred. No.: 9,58e-181 Length: 908
Score: 2328.00 Matches: 430
Percent Similarity: 85.34% Conservative: 53
Best Local Similarity: 75.97% Mismatches: 81
Query Match: 70.48% Indels: 2
Gaps: 2
DB:
US-10-828-332-6 (1-1755) x US-08-823-110-1 (1-908)
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327	GlyAlaValThrIleLeuProIysArgAlaSerIleAspGlyPheAspArgTyrPheArg	346
64	AGCCGCACGCTGGACAACAACAGAGCGCAACATCTGGTTTGGCCGAGTTCTGGAGGACAAC	123
347	SerArgThrLeuAlaAsnAsnArgAsnValTyrPheAlaGluPheTyrGluGluAsn	366
124	TTCCATTGCAAGTTGAGCCGCCACGCGCTCAAGAAGGAAGCAACATCAAGAAGTGCACC	183
367	PheGlyCysIysLeuGlySerHisGly---LysArgAsnSerHisIleLysLysCysThr	385
184	AACGAGAGCGCATCGGCAGGACTCGCCCTATGACGAGGAGGGAGGTCAGTTGCTG	243
386	GlyLeuGluArgIleAlaArgAspSerSerTyrGluGlnGluGlyLysValGlnPheVal	405
244	ATTGACGCTGTGATCGCCATCGGCACGCGCTGCACGCAATGACCGGTACCTGTGTCCC	303
406	IleAspAlaValTyrSerMetAlaTyrAlaLeuHisAsnMetHisLysAspLeuCysPro	425
304	GGCCGCTGAGACTCTGCCCTCGCATGAGACCCCGCTGGATGGACCCAGCTCTTAAAGTAC	363
426	GlyTyrIleGlyLeuCysProArgMetSerThrIleAspGlyLysGluLeuLeuGlyTyr	445
364	ATCAGGAACGTCACATCTCAGGCATTCGCGGGAAACCTGTAACTTCAATGACAACGGA	423
446	IleArgAlaValAsnPheAsnGlySerAlaGlyThrProValThrPheAsnGluAsnGly	465
424	GACGCACGGGCGCTACGACATCTACCAGTACCACACTGCGCAATGGCTGGCCGAGTAC	483
466	AspAlaProGlyArgTyrAspIlePheGlnTyrGlnIleThrAsnLysSerThrGluTyr	485
484	AAGGTCATCGGCTCGTGACACAGACCACTGCACCTCAGAAATAGAGCGGATGACGTGCCA	543
486	LysValIleGlyHisTyrThrAsnGlnLeuHisLeuLysValGluAspMetGlnTyrAla	505
544	GGGAGTGGCCAGAGCTCCGCGCTCCATCTGCAGTCTGCCCTCCAGCCCGCGGAGCGGA	603
506	HisArgGluHisThrHisProAlaSerValCysSerLeuProCysLysProGlyGluArg	525
604	AAGAAGACTGTGAAGGCACTGGCTTGTCTGGCACTGCAGCTCCGAGCCCTGCACCGGCTACCAG	663
526	LysLysThrValLysGlyValProCysCysTrpHisCysGluArgCysGluGlyTyrAsn	545
664	TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCCCTACGACATCGCGGCCACAGAGAAC	723
546	TyrGlnValAspGluLeuSerCysGluLeuCysProLeuAspGlnArgProAsnMetAsn	565
724	CGCACGAGCTGCCAGCCCATCCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGCCGCTG	783
566	ArgThrGlyCysGlnLeuIleProIleLysLeuGluTyrHisSerProTyrPheAlaVal	585
784	CTGCCCTCTTCTCGGCGCTGGTGGGATCGCCGCCACGCTGTTTCGTTGGTGGTCCACGTTT	843
586	ValProValPheValAlaIleLeuGlyIleIleAlaThrThrPheValIleValThrPhe	605
844	GTGCGCTACACGATACCCCATCGTCAAGGCGCTCGCGCGCGGAACTGAGCTACGTCGTG	903
606	ValArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrValLeu	625
904	CTGCGGGGCATCTTTCTGTGCTACGCCCATCACTTCTCTCATGATCGCAGAGCCGACCTG	963
626	LeuThrGlyIlePheLeuCysTyrSerIleThrPheLeuMetIleAlaProAspThr	645
964	GGGACCTGTTGCTCCCGCCCATCTTCTAGGCGCTCGGCATGATGATCATGCTAGCGGCC	1023
646	IleIleCysSerPheArgArgValPheLeuGlyLeuGlyMetCysPheSerTyrAlaAla	665
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666	LeuLeuThrLysThrAsnArgIleHisArgIlePheGluGlnGlyLysSerValThr	685
1084	GCCTCCGCTTTCATCAGCCCGGCTCGCAGCTGGCCATCACTTTCATCTCATCTCCCTG	1143

Db	652	ValAlaValCysSerPheArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla	671
Qy	1021	GCCCTGCTGACCAAGACCAACCGCATTTACCGCATCTTCAGCAGGCGCAACCGTCGGTC	1080
Db	672	AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysLysSerVal	691
Qy	1081	AGTGCCCGCGTTTCATCAGCCCGCGCTCGCAGCTGGCCATCACTTCATCTCATCTCC	1140
Db	692	ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer	711
Qy	1141	CTGCAGCTGCTGGCATCTCGGTGTGTTCTGTGTGTGACCCCTCCCACTCGGTGTGGAC	1200
Db	712	ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProAsnIleIleIleAsp	731
Qy	1201	TTCCAGGACCAACGGACACTTGACCCCGCTTTGCCAGGGCGGTCTCAAGTGGACATC	1260
Db	732	TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle	751
Qy	1261	TCGGACCTGTCCCTCATCTGCTGCTGGGCTACAGCATGCTGCTGATGGTCACGTGTACT	1320
Db	752	ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr	771
Qy	1321	GTGTACGCCATCAAGACCGAGGGGTGCCCGAGACCTTCAACGAGGCGCAAGCCCATCGGC	1380
Db	772	ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly	791
Qy	1381	TTCCACCATGTACACCACCTGCATTGTCTGGCTGGCTTCATCCCATCTTTTGGCACC	1440
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Qy	1441	TCAGTTCAGCGCAACAGCTGTACATCCAGAACACCACTTGACGGGTCTCCGTGAGTCTG	1500
Db	812	AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrLeuThrIleSerMetAsnLeu	831
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Db	832	SerAlaSerValAlaLeuLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHis	851
Qy	1561	CCGAGCAGAACGTGCCCAAGCGGACCGAGCTCAAGCCGTGTGTACCGCGGCCACC	1620
Db	852	ProGluLeuAsnValGlnLysArgLysArgSerPheLysAlaValValThrAlaAlaThr	871
Qy	1621	ATGTCCAAAGTTCCACAGAGGGGCACTTCAGGCGCAATGGGGAAGCAATACAGAG	1680
Db	872	MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu	891
Qy	1681	CTGTGTGAGAACCTGGAGACCCCAAGCGCTGGCTACCAAAACAGCTACGTCACTACACC	1740
Db	892	LeuCysGluAsnValAspProAsnSerProAlaAlaLysLysLysTyrValSerTyrAsn	911
Qy	1741	AACCATGCCATC	1752
Db	912	AsnLeuValIle	915

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; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,734A
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-452-734A-2

Alignment Scores:
Pred. No.: 3,77e-171
Score: 2210.00
Percent Similarity: 82.53%
Best Local Similarity: 69.52%
Query Match: 66.91%
DB: 2
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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Qy	841	TTTGTGCGCTACAAAGATACCCCATCGTCAAGCGCTCGGCGCGGAACGTAGCTACGTG	900
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Qy	1021	GCCTGTGTACCAAGACCAACCGCATTTACGCATCTTTGAGCAGGCGCAACGGTGGGTC	1080
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Db	712	ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProProAsnIleIleIleAsp	731
Qy	1201	TTCCAGGACCAACGGACACTGTGACCCCGCTTTGCCAGGGCGGTGTCAAGTGGCAATC	1260
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Db	812	AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrThrLeuThrIleSerMetAsnLeu	831
Qy	1501	AGGCTTTCAGTGTCCCTGGGAGTCTCTACATGCGCCAAAGTCTACATCATCTCTTCCAC	1560
Db	832	SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHis	851
Qy	1561	CCGAGCAGAACTGTGCCCAAGCGCAAGCGCATCTCAAAGCGGTGTGTCAACGGCGCCAC	1620
Db	852	ProGluLeuAsnValGlnLysArgLysArgSerPheLysAlaValValThrAlaAlaThr	871

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Qy 1681 CTGTGTGAGAACCTGGAGAGCCCCAGGCGCTGGCTACCAAAACAGACCTACGTCACCTACAC 1740
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RESULT 13
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; Sequence 2, Application US/08176401B
; Patent No. 6274330
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,401B
; FILING DATE: 30-DECEMBER-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-401B-2

Alignment Scores:
Pred. No.: 3,77e-171 Length: 915
Score: 2210.00 Matches: 406
Percent Similarity: 82.53% Conservatve: 76
Best Local Similarity: 69.52% Mismatches: 100
Query Match: 66.91% Indels: 2
DB: 3 Gaps: 2

US-10-828-332-6 (1-1755) x US-08-176-401B-2 (1-915)

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Alignment Scores:

Pred. No.: 3,776-171 Length: 915
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US-10-828-332-6 (1-1755) x PCT-US94-14989-2 (1-915)

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Db 492 TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAenIleGluAspMetGlnTrp 511
QY 541 CCAGGAGTGGCGAGCGCTCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCCGGGAG 600
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QY 1681 CTGTGTGAGAACCTGGAGACCCCGCTGCTACCAACACAGACCTAGCTACCTACACCC 1740
Db 892 LeuCysGluAenValAspProAsnSerProAlaAlaLysLysLysTyrValSerTyrAen 911
QY 1741 AACCATGCCATC 1752
Db 912 AsnLeuValIle 915

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RESULT 15

US-08-617-785-4
 ; Sequence 4, Application US/08617785E
 ; Patent No. 6228610
 ; GENERAL INFORMATION:
 ; APPLICANT: Flor, Peter J.
 ; APPLICANT: Kuhn, Rainer
 ; APPLICANT: Lindaur, Kristen
 ; APPLICANT: Futtner, Irene
 ; APPLICANT: Knopfel, Thomas
 ; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
 ; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
 ; FILE REFERENCE: 4-19679/A/PCT
 ; CURRENT APPLICATION NUMBER: US/08/617,785E
 ; FILING DATE: 1996-03-19
 ; EARLIER APPLICATION NUMBER: PCT/EP94/02991


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; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-4

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Alignment Scores:

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Pred. No.: 1 18e-169 Length: 867
Score: 2191.50 Matches: 405
Percent Similarity: 81.85% Conservative: 73
Best Local Similarity: 69.35% Mismatches: 99
Query Match: 66.35% Indels: 7
DB: 3 Gaps: 3

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US-10-828-332-6 (1-1755) x US-08-617-785-4 (1-867)

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QY 7 GGGGTATCATCTCTTCCCAACGAGGATGACA---TCAGGGTTTCGACCGCATCTCTCC 63
DB 277 GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaTyrPheThr 296
QY 64 AGCCGCAAGTGGACAAACAGGCGCAACATCTGTTGTCGAGTCTCGGAGGACAAAC 123
DB 297 SerArgThrLeuGluAsnAsnArgAsnValTyrPheAlaGluTyrTrpGluGluAsn 316
QY 124 TTCCATTCCAGTTGAGCGGCACCGCTCAAGAGGAAGCCACATCAAGATGACCC 183
DB 317 PheAsnCysLysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr 336
QY 184 AACCCAGAGCGCATCGGCGAGCTCGGCTATGAGCAGGAGGGAAGCTGCAGTTCGTG 243
DB 337 GlyGlnGluArgIleGlyLysAspSerAsnTyrGluGlnGluGlyLysValGlnPheVal 356
QY 244 ATTGACGTGTGTACGCCATGGCCACCGCTGACGCCATCGACCGTGTGTGTCC 303
DB 357 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisMetAsnLysAspLeuLysAla 376
QY 304 GGCCGCTAGACTCTGCTCGCATGACACCCCGTGGATGACCCACCTGCTTAAGTAC 363
DB 377 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyLysLeuLeuLysTyr 396
QY 364 ATCAGGAACGTCAACTCTCTCAGGCAATGCGGGAAACCTGTAAACCTTCAATGAGAACGGA 423
DB 397 IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 416
QY 424 GACGACCGGGCGCTACGACATCTACAGTACCAACTGCGCAATGGCTCG---GCCGAG 480
DB 417 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrThrAsnThrSerAsnProGly 436
QY 481 TACAGGTATCGGCTCGTGGACAGACACCTGACCTCAGAAATAGACGGATGACAGTGG 540
DB 437 TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 456
QY 541 CCAGGAGTGGCGACAGCTCGCGCTCCATCTCAGCTCTGCCCTGCGAGCCGGGGAG 600
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QY 721 AACCCGACGAGTGGCGACGCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGGTGGCC 780

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Db 517 AsnArgThrGlyCysGlnAspIleProIleIleLysLeuGluTrpHisSerProTrpAla 536
QY 781 GTGCTGCCCTCTCTCCGCGCTGGTGGATCGCCCGCCAGCTGTTCGTGGTGGTACG 840
Db 537 ValIleProValPheLeuAlaMetLeuGlyIleAlaThrIlePheValMetAlaThr 556
QY 841 TTTGTGGCTACCAACGATACCCCATCGTCAAGCGCTTCGGCGCGGAACTAGACTAGTG 900
Db 557 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 576
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Db 577 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 596
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Db 817 MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu 836
QY 1681 CTGTGTGAGAACCTGGAG-----ACCCGAGCGCTGGCTTACCAACAGAC 1725
Db 837 LeuCysGluAsnValAspProAsnAsnCysIleProProValArgLysSerValGlnLys 856
QY 1726 TACGTCACTTAC 1737
Db 857 SerValThrTrp 860

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Search completed: June 17, 2005, 18:55:27
Job time : 111 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 17, 2005, 18:18:26 ; Search time 254 Seconds

(without alignments)

5344.602 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 3303

Sequence: 1 atgcaggggtatcatc.....acacacacatgccatctag 1755

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Fgapext 7.0			
Delop 6.0			
Delext 7.0			

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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8: Genesecp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107	94.1	584	6 ABR56244	Abg56244 Rat gluta
2	3050.5	92.4	604	6 ABR74133	Abg74133 Rat metab
3	3050.5	92.4	912	7 ADE58164	Ades8164 Rat Prote
4	3050.5	92.4	912	7 ADE58168	Ades8168 Rat Prote
5	3017	91.3	909	8 ADO29095	Ado29095 Mouse nov
6	3004.5	91.0	909	5 AAO15101	Aao15101 Human ph8
7	3004.5	91.0	912	2 AAR82658	Aar82658 Human mgl
8	3004.5	91.0	912	5 AAE23757	Aae23757 Human met
9	3004.5	91.0	912	6 ABR81846	Abp81846 Human met
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13	3004.5	91.0	912	8 ADO89114	Ado89114 Human uro
14	3001.5	90.9	912	2 AAR72092	Aar72092 Human mgl
15	2912.5	88.2	591	8 ADR08623	Adr08623 Human pro
16	2852.5	86.4	886	8 ABM84666	Abm84666 Human dia
17	2752.5	83.3	796	8 ADR10452	Adr10452 Human pro
18	2752	83.3	862	8 AEM84667	Am84667 Human dia
19	2711	82.1	1422	5 AAO15102	Aao15102 Human phm
20	2377	72.0	908	6 ABR62488	AbR62488 Human met
21	2377	72.0	908	6 ABR62489	AbR62489 Human met
22	2377	72.0	908	8 ADO29476	Ado29476 Human GPC
23	2374	71.9	908	6 ABR62490	AbR62490 Human met
24	2370	71.8	908	2 AAW41568	Aaw41568 Human met
25	2370	71.8	908	5 ABB09564	Abb09564 Human GRM
26	2370	71.8	908	6 ABR81850	Abp81850 Human met
27	2370	71.8	908	7 ADE31729	Ades31729 Human 255
28	2370	71.8	908	8 ADO89128	Ado89128 Human uro
29	2369	71.7	908	6 ABR62491	AbR62491 Human met
30	2348	71.1	1142	4 ABR29451	Abg29451 Novel hum
31	2336	70.7	908	8 ADO29477	Ado29477 Mouse GPC
32	2328	70.5	908	2 AAW49928	Aaw49928 Human met.
33	2328	70.5	913	4 ABR29452	Abg29452 Novel hum
34	2319	67.2	915	5 ABR62492	Abg62492 Human GPC
35	2319	67.2	915	6 ABR81849	Abp81849 Human met
36	2219	67.2	915	7 ADE55969	Ades55969 Human Pro
37	2219	67.2	915	7 ADJ93191	Adj93191 Human met
38	2219	67.2	915	8 ADO29103	Ado29103 Human nov
39	2215	67.1	915	2 AAR72097	Aar72097 Human mgl
40	2214	67.0	915	5 ABR95164	Abg95164 Human GPC
41	2214	67.0	915	8 ADO29104	Ado29104 Mouse nov
42	2213	67.0	915	5 ABR95165	Abg95165 Human GPC
43	2212	67.0	915	5 ABR95166	Abg95166 Human GPC
44	2210	66.9	915	2 AAR80479	Aar80479 Rat metab
45	2210	66.9	915	6 AAE30199	Aae30199 Rat metab

ALIGNMENTS

RESULT 1

ABR56244

ID ABR56244 standard; protein; 584 AA.

XX AC ABR56244;

XX XX 20-NOV-2003 (first entry)

XX DT 20-NOV-2003 (first entry)

XX DE Rat glutamic acid receptor.

XX XX Rat; anorectic; antiulcer; antidiabetic; laxative; antidiarrheic;

KW glutamic acid receptor; receptor; gastrointestinal tract disorder;

KW sitieigia; obesity; ulcer; diabetes; constipation; diarrhoea.

XX OS Rattus norvegicus.

XX XX WO2003035873-A1.

XX PN 01-MAY-2003.

XX PD 23-OCT-2002; 2002WO-JP010984.

XX PF 23-OCT-2001; 2001JP-00325159.

XX PR (AJIN) AJINOMOTO CO INC.

XX XX San Gabriel A, Maekawa T, Uneyama H, Torii K;

XX WPI; 2003-430418/40.

XX N-PSDB; ACC70676.

XX PT Novel glutamic acid receptor protein and encoded DNA, applicable in

PT screening agonists or antagonists of glutamic acid or allosteric

PT modulator for use as drugs in ameliorating symptoms and diseases e.g.

PT	obesity.	Db	221	GlnTyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGlu	240
XX					
PS	Claim 3; Page 33-35; 39pp; Japanese.	QY	721	AACGGCAGAGCTGCCAGCCCATCCCATCGTGAAGTTGGAGTGGGACTCGCCGTGGGCC	780
XX					
CC	The present sequence is the protein sequence for rat glutamic acid	Db	241	AsnArgThrSerCysGlnProIleValLysLeuGluThrPheAspSerProThrAla	260
CC	receptor. The receptor has a transmembrane domain and an intracellular				
CC	domain common to type 4 metabotropic glutamic acid receptor protein, and	QY	781	GTGTCGCCCTCTCTCTGGCGGTGGGCGATCCCGCCACGCTGTCGTGGTGGTTCACG	840
CC	an extracellular domain shorter by 316 or 327 amino acid residues than				
CC	type 4 metabotropic glutamic acid receptor protein. The receptor and its	Db	261	ValLeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThr	280
CC	coding sequence are useful in screening agonists or antagonists of	QY	841	TTTGTGCGCTACAAACATACCCCATCGTCAAGCCCTCGGCGCGGAACAGTACGTG	900
CC	glutamic acid or allosteric modulator for use as drugs in ameliorating				
CC	symptoms and diseases due to abnormal metabolism in gastrointestinal	Db	281	PheValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrVal	300
CC	tract including small and large intestines e.g. sitieirgia, obesity,				
CC	ulcer, diabetes, constipation and diarrhoea	QY	901	CTGCTGGGGGCGATCTTCTGTGTAGCCCATCTACTCTCTCATGATCGGAGCCGGAC	960
XX					
SQ	Sequence 584 AA;	Db	301	LeuLeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAsp	320
	Alignment Scores:	QY	961	CTGGGAGACCTGTTCTCGCTCCGCGCATCTTCTTAGGGCTCGGCATGAGCATCAGCTACGCG	1020
	Pred. No.: 9,04e-217 Length: 584	Db	321	LeuGlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAla	340
	Score: 3107.00 Matches: 584				
	Percent Similarity: 100.00% Conservative: 0	QY	1021	GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTAGCAGGCGAAACGTCGTGTC	1080
	Best Local Similarity: 100.00% Mismatches: 0				
	Query Match: 94.07% Indels: 0	Db	341	AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerVal	360
	DB: 6 Gaps: 0				
	US-10-828-332-6 (1-1755) x ABR56244 (1-584)	QY	1081	AGTCCCGCGGCTTTTCATCAGCCGCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCC	1140
		Db	361	SerAlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSer	380
		QY	1141	CTGCAGCTGCTCGCGCATCTGCGTGTGGTTCGTGGTGACCCCTCCCATCTCGGTGGTGGAC	1200
		Db	381	LeuGlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAsp	400
		QY	1201	TTCCAGGACCAACCGACACTTGACCCCGCTTTCCAGGGCGGTCTCAAGTCGACATC	1260
		Db	401	PheGlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIle	420
		QY	1261	TCGGACCTGTCCCTCATCTGCGTCTGGCTGACAGCATGCTGTGATGGTTCACCTGTACT	1320
		Db	421	SerAspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThr	440
		QY	1321	GTGTACGCCATCAAGACCCGAGGGGTGCCGAGACCTTCAACGAGGCGCAAGCCCATCGGC	1380
		Db	441	ValTyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGly	460
		QY	1381	TTCAACATGTACACCACTGCATTTGCTGGCTGGCTTCATCCCATCTTTTGGGACAC	1440
		Db	461	PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr	480
		QY	1441	TCACAGTCACGCCGACAGCTGTACATCCAGACACACACTGACGGTCTCCGTGAGTCTG	1500
		Db	481	SerGlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeu	500
		QY	1501	AGCCGTTTCAGTGTCCCTGGGGATCTCTACATGCCCCAAAGCTTACATCATCTCTTCCAC	1560
		Db	501	SerAlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHis	520
		QY	1561	CCGGAGCAGAACGTGCCCAAGCGCAAGCGAGTCTCAAAGCGGTGGTTCACCGCGCCAC	1620
		Db	521	ProGluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThr	540
		QY	1621	ATGTCCCAACAGTTTCACAGAGGGCACTTCAGGCCCCATTCGGAGCGGAGCCAAATCAG	1680
		Db	541	MetSerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGlu	560
		QY	1681	CTGTGTGAGAACCTGGAGACCCCGCGCTGCTGCTACCAACAGACCTACGTTCACCTACAC	1740
		Db	561	LeuCysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrThr	580
		QY	1741	AACCATGCCATC 1752	
		Db	581	AsnHisAlaIle 584	

PT	obesity.	Db	221	GlnTyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGlu	240
XX					
PS	Claim 3; Page 33-35; 39pp; Japanese.	QY	721	AACGGCAGAGCTGCCAGCCCATCCCATCGTGAAGTTGGAGTGGGACTCGCCGTGGGCC	780
XX					
CC	The present sequence is the protein sequence for rat glutamic acid	Db	241	AsnArgThrSerCysGlnProIleValLysLeuGluThrPheAspSerProThrAla	260
CC	receptor. The receptor has a transmembrane domain and an intracellular				
CC	domain common to type 4 metabotropic glutamic acid receptor protein, and	QY	781	GTGTCGCCCTCTCTCTGGCGGTGGGCGATCCCGCCACGCTGTCGTGGTGGTTCACG	840
CC	an extracellular domain shorter by 316 or 327 amino acid residues than				
CC	type 4 metabotropic glutamic acid receptor protein. The receptor and its	Db	261	ValLeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThr	280
CC	coding sequence are useful in screening agonists or antagonists of	QY	841	TTTGTGCGCTACAAACATACCCCATCGTCAAGCCCTCGGCGCGGAACAGTACGTG	900
CC	glutamic acid or allosteric modulator for use as drugs in ameliorating				
CC	symptoms and diseases due to abnormal metabolism in gastrointestinal	Db	281	PheValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrVal	300
CC	tract including small and large intestines e.g. sitieirgia, obesity,				
CC	ulcer, diabetes, constipation and diarrhoea	QY	901	CTGCTGGGGGCGATCTTCTGTGTAGCCCATCTACTCTCTCATGATCGGAGCCGGAC	960
XX					
SQ	Sequence 584 AA;	Db	301	LeuLeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAsp	320
	Alignment Scores:	QY	961	CTGGGAGACCTGTTCTCGCTCCGCGCATCTTCTTAGGGCTCGGCATGAGCATCAGCTACGCG	1020
	Pred. No.: 9,04e-217 Length: 584	Db	321	LeuGlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAla	340
	Score: 3107.00 Matches: 584				
	Percent Similarity: 100.00% Conservative: 0	QY	1021	GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTAGCAGGCGAAACGTCGTGTC	1080
	Best Local Similarity: 100.00% Mismatches: 0				
	Query Match: 94.07% Indels: 0	Db	341	AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerVal	360
	DB: 6 Gaps: 0				
	US-10-828-332-6 (1-1755) x ABR56244 (1-584)	QY	1081	AGTCCCGCGGCTTTTCATCAGCCGCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCC	1140
		Db	361	SerAlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSer	380
		QY	1141	CTGCAGCTGCTCGCGCATCTGCGTGTGGTTCGTGGTGACCCCTCCCATCTCGGTGGTGGAC	1200
		Db	381	LeuGlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAsp	400
		QY	1201	TTCCAGGACCAACCGACACTTGACCCCGCTTTCCAGGGCGGTCTCAAGTCGACATC	1260
		Db	401	PheGlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIle	420
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		QY	1381	TTCAACATGTACACCACTGCATTTGCTGGCTGGCTTCATCCCATCTTTTGGGACAC	1440
		Db	461	PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr	480
		QY	1441	TCACAGTCACGCCGACAGCTGTACATCCAGACACACACTGACGGTCTCCGTGAGTCTG	1500
		Db	481	SerGlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeu	500
		QY	1501	AGCCGTTTCAGTGTCCCTGGGGATCTCTACATGCCCCAAAGCTTACATCATCTCTTCCAC	1560
		Db	501	SerAlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHis	520
		QY	1561	CCGGAGCAGAACGTGCCCAAGCGCAAGCGAGTCTCAAAGCGGTGGTTCACCGCGCCAC	1620
		Db	521	ProGluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThr	540
		QY	1621	ATGTCCCAACAGTTTCACAGAGGGCACTTCAGGCCCCATTCGGAGCGGAGCCAAATCAG	1680
		Db	541	MetSerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGlu	560
		QY	1681	CTGTGTGAGAACCTGGAGACCCCGCGCTGCTGCTACCAACAGACCTACGTTCACCTACAC	1740
		Db	561	LeuCysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrThr	580
		QY	1741	AACCATGCCATC 1752	
		Db	581	AsnHisAlaIle 584	

QY 364 ATGAGAACGCTCAACTTCTCAGGATTCGGGGAACCCCTGTAACTTCAATGAGACGGA 423
DB 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAenGly 469
QY 424 GAGCCACCGGGCGCTACGACATCTACCACTGCACTGCGCAATGCGCTCGCGCGAGTAC 483
DB 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 489
QY 484 AAGGTCAATCGGCTCGTGAGCAGACCACTGCACCTCAGAAATAGAGCGGATGCAAGTGGCCA 543
DB 490 LysValIleGlySerThrAspHisLeuHisLeuAargIleGluAargMetGlnTrpPro 509
QY 544 GGGAGTGGCAGAGCTCGCGCTCATCTGAGTCTGCGCTGCGCAGCCGCGGGAGCGA 603
DB 510 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
QY 604 AAGAAGACTGTGAAGGCGATGCTGCTGCTGCGCACTGCGAGCCCTGCACCGGGTACCAG 663
DB 530 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 549
QY 664 TACCAAGTGACCGCTACACCTGTAAAGACCTGCCCTTACGACATGCGGCCCAACAGAGAAC 723
DB 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
QY 724 CGCAGAGCTGCGAGCCCATGCCATCGTCAAGTTCGAGTGGGACTCGCGCTGGCGCGTG 783
DB 570 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 589
QY 784 GTGCGCTTCTTCTGCGCGCTGGGCGCATCGCGCCACGCTGTTCTGCTGCTGCTGCTGCT 843
DB 590 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 609
QY 844 GTGCGCTACAAACATACCCCATCGTCAAGGCTCGCGCGCGGAACTGAGCTACGCTGCTG 903
DB 610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
QY 904 GTGCGCGGATCTTCTGTGTACGCCACTTACCGCATCTTCTCATGATCGCAGCGCGACCTG 963
DB 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
QY 964 GGGACCTGTCTGCTCGCGCATCTTCTTAGGCTCGGCGATGAGCATGAGTACGCGGCC 1023
DB 650 GlyThrCysSerLeuArgGlyIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
QY 1024 CTGCTCACCAGAACCGCATTTTACCGCATCTTTGAGCAGGGCAACCGTGGTCACT 1083
DB 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
QY 1084 GCCCGCGTTTCATCAGCCCGGCTCGCAGCTGGCCATCACCTTCATCTCATCTCCCTG 1143
DB 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 709
QY 1144 CAGCTGCTGGCATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1203
DB 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
QY 1204 CAGGACCAACGAGACTTCACCCCGCTTTCAGGGCGCTGCTCAAGTGGCAGCATCTCG 1263
DB 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
QY 1264 GACCTGTCTCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1323
DB 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
QY 1324 TAGCCCATCAGACCGAGCGTGGCCGAGACTTCAACAGAGCGCAAGCCCATCGGCTTC 1383
DB 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
QY 1384 ACCATGTACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
DB 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 809

QY 1444 CAGTCAGCGCAGCAAGCTGTATCATCCAGACCAACCACTGACCGGTCTCCGTGAGTCTGAGC 1503
DB 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 829
QY 1504 GCTTCAGTGTCTCCCTGGGATGCTTACATGCCCAAGTCTACATCATCTCTTCCACCCG 1563
DB 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro 849
QY 1564 GAGCAGAACGTGCCCAAGCGCAAGCGAGTCTTCAAAGCGGTGTCACCCCGCCACCATG 1623
DB 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 869
QY 1624 TCCACAAAGTTTCACACAGAGCGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG 1683
DB 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
QY 1684 TGTGAGAACCTGAGACCCCGCTGCTGCTACCAACAGACCTTACCTACCTACACCAAC 1743
DB 890 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
QY 1744 CATGCCATC 1752
DB 910 HisAlaIle 912
RESULT 4
ADE58168
ID ADE58168 standard; protein; 912 AA.
XX ADE58168;
AC ADE58168;
XX 29-JAN-2004 (first entry)
DT Rat Protein P31423, SEQ ID NO 4039.
DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0345382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P31423.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially

expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [ftp.wipo.int/pub/published/bct/sequences](http://wipo.int/pub/published/bct/sequences).


```
QY 724 CGCAGAGCTGCGACCCATCCCATCTCAAGTTGGAGTGGAGCTCGCGTGGCGCTG 783
Db 567 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProtrAlaVal 586
QY 784 CTGCGCCCTCTTCTCGCGCTGGTGGCATCGCGCCAGCTGTTCTGTTGTTGTCACGTTT 843
Db 587 LeuProLeuPheLeuAlaValValGlyIleAlaIleThrLeuPheValValThrPhe 606
QY 844 GTGCGCTCAACAGATACCCCATCTCAAGGCTCGGCGCGGAACTGAGCTACGTGCTG 903
Db 607 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 626
QY 904 CTGCGGGCATCTTTCTGTGCTACGCCACTACCTTCCTCATGATCGCAGAGCCGACCTG 963
Db 627 LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 646
QY 964 GGGACTGTTCTCGCGCGCATCTTCTTAGGCTCGGCATGAGCATCAGCTACGCGGCC 1023
Db 647 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 666
QY 1024 CTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCGGGCAAAAGGTGCTCAGT 1083
Db 667 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 686
QY 1084 GCCCGCGCTTTCATCAGCCGGCGCTCGAGCTGGCGCATCACCTTCATCTCATCTCCCTG 1143
Db 687 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheValIleSerLeu 706
QY 1144 CAGCTGCTCGGCATCTGCGTGGTTCGTGGTGGACCCCTCCCATCTGGTGGTGTGACTTC 1203
Db 707 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 726
QY 1204 CAGGACCAACGACACTTGACCCCGCTTTGCCAGGGCGTGTCAAGTGGACATCTCG 1263
Db 727 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 746
QY 1264 GACCTGTCCCTCATCTGCTGCTGGCTACAGCATGCTGCTGATGGTCACGTACTGTG 1323
Db 747 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 766
QY 1324 TACGCGCATCAAGACCGAGCGCTGCCGAGACTTCAACAGGCCCAAGCCATCGGCTTC 1383
Db 767 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 786
QY 1384 ACCATGTACACCTGCAATGCTGTGCTGGCTTCATCCCATCTTTTGGCACCTCA 1443
Db 787 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 806
QY 1444 CAGTCAGCGCAGACTGTACATCCAGACCAACCACTGACGCTCGGTGAGTCTGAGC 1503
Db 807 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 826
QY 1504 GCTTCAGTGTCCCTGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCACCCG 1563
Db 827 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 846
QY 1564 GAGCAGAACGTCGCCAAGCGCACAGTCTCAAGGCGTGGTCAACGCCGCCACCATG 1623
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QY 1624 TCCACACAGTTCACACAGAGGGCACTTCAGGCCCAATGGGAGCCCAATCAGAGCTG 1683
Db 867 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 886
QY 1684 TGTGAGAACCTGGAGACCCGCTGGCTTACCAACAGACCTAGCTCACCTACACCAAC 1743
Db 887 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrAsn 906
QY 1744 CATGCCATC 1752
Db 907 HisAlaIle 909
```

RESULT 6

AAO15101
ID AAO15101 standard; protein; 909 AA.

XX AAO15101;

AC AC

29-AUG-2003 (revised)

DT 22-AUG-2002 (first entry)

XX Human phsPmGluR4 chimeric protein.

DE Human; G-protein fusion receptor; extracellular domain;

XX transmembrane domain; intracellular domain; Car; mGluR; GABABR;

KW modulator identification.

XX Homo sapiens.

OS Chimeric.

XX WO200229033-A2.

PN 11-APR-2002.

XX 03-OCT-2001; 2001WO-US031074.

XX 03-OCT-2000; 2000US-00679664.

PR (NPSP-) NPS PHARM INC.

XX Stormann T, Hammerland LG, Storjohann LL, Busby JG, Garrett JE;

XX Simin RT;

PI WPI; 2002-330170/36.

DR Novel G-protein fusion receptor, useful for identifying modulators of

XX Car, mGluR and GABABR, comprises G-protein joined to the intracellular

XX domain of the receptor.

PS Disclosure; Fig 16; 168pp; English.

CC The invention comprises G-protein fusion receptors - comprising
CC extracellular, transmembrane and intracellular domains similar to Car,
CC mGluR or GABAB receptor sequences. The G-protein fusion receptors of the
CC invention may also possess a linker joined to the carboxy terminus of the
CC intracellular domain, and a G-protein joined to the linker. The G-protein
CC fusion receptors of the invention are useful for identifying modulators
CC of Car, mGluR and GABABR for use in treating associated conditions. The
CC present amino acid sequence was used in the production of the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 909 AA;

Alignment Scores:

Pred. No.: 2.8e-209 Length: 909
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 90.96% Indels: 1
DB: 5 Gaps: 1

US-10-828-332-6 (1-1755) x AAO15101 (1-909)

QY 7 GGGGTATCATCTTTGGCCAAACGAGGATGACA--TCAGGGTTCCAGCCGATCTTCTCC 63

Db 327 GlyAlaValThrIleLeuProLysArgMetSerValargGlyPheAspArgTyrPheSer 346

QY 64 AGCCGACGCTGGACAAACACAGCGCAACATCTGTTGCGGAGTTCTGGAGGACAAAC 123

Db 347 SerArgThrLeuAspAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 366

QY 124 TTCATTGCAAGTTGAGCGCCGCTCAGAGGAGGAGCCATCAAGAGTGCACC 183

Db 367 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysCysThr 386

QY 184 AACGAGAGCGCATCGGCGAGGACTCGGCTATGACGAGGAGGGAAGGTGCGTTCGTG 243
 Db 387 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 406
 QY 244 ATTGACGCTGTGTACGCGCATCGGCGCCAGCGCTGCACGCCATGACCGTGCACCTGTCTCC 303
 Db 407 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCyPro 426
 QY 304 GCGCGGTAGGACTTCGCTCCGCTCGCATGAGACCCCGTGGATGGCACCCAGCTGCTTAAGTAC 363
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 QY 364 ATCAGAAAGTCAACTCTCAGGCATTCGGGGAACCCCTGTAACCTTCAATGAGAACGGA 423
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 QY 424 GACGACCGGGCGCTACGACATCTACCACTGCACTGCGCAATGCTCGGCGGAGTAC 483
 Db 467 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 486
 QY 484 AAGGTCAATCGGCTCGTGGACAGACCACTGCACCTCAGAAATAGAGCGGATGCAGTGGCCA 543
 Db 487 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 506
 QY 544 GGGAGTGGCCAGAGCTCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCCGGGAGCGA 603
 Db 507 GlySerGlyGlnGlnLeuProArgSerIleCySerLeuProCysGlnProGlyGluArg 526
 QY 604 AAGACACTGTGAAGGGCATGGCTCTGCTGCACTGCGAGCCCTGCACCGGTTACAC 663
 Db 527 LysLeuThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 546
 QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACTCGCCCTACGACATCGCGCCGCGCCACAGAAC 723
 Db 547 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 566
 QY 724 CGCACGAGCTGCAGCCCATCCCATCGTCAAGTGGAGTGGGACTCGCGCGCGCG 783
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 Db 687 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 706
 QY 1144 CAGTCTCGGCATCTGCGTGGTTCGTGGTGGACCCCTCCCACTCGGTGGTCACTTC 1203
 Db 707 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 726
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Db 747 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 766
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 Db 827 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 846
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 Db 847 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 866
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 Db 867 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 886
 QY 1684 TGTGAGAACCCTGGAGACCCCGCTGCTGCTACCAACAGACCTGCTACCTACCTACCAAC 1743
 Db 887 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 906
 QY 1744 CATGCCATC 1752
 Db 907 HisAlaIle 909
 RESULT 7
 AAR82658
 ID AAR82658 standard; protein; 912 AA.
 XX
 AC AAR82658;
 XX
 DT 20-DEC-1995 (first entry)
 XX
 DE Human mGluR4.
 XX
 KW Metabotropic glutamate receptor 4; mGluR4; stroke; epilepsy;
 KW Alzheimer disease; detection; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Domain
 FT
 FT Location/Qualifiers
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 FT /label= TMD-I
 FT /note= "transmembrane domain I"
 FT 625..645
 FT /label= TMD-II
 FT /note= "transmembrane domain II"
 FT 657..675
 FT /label= TMD-III
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 FT 699..720
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 FT /note= "transmembrane domain VI"
 FT 823..847
 FT /label= TMD-VII
 FT /note= "transmembrane domain VII"
 FT XX

QY 1624 TCACAAAGTTCACACAGAGGCGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG 1683
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 QY 1684 TGTGAGAACTCGAGACCCAGCGCTGCTACCAACAGACACTACCTACCTACACCAAC 1743
 DB 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 909
 QY 1744 CATGCCATC 1752
 DB 910 HisAlaIle 912
 RESULT 8
 ID AAE23757
 XX AAE23757 standard; protein; 912 AA.
 AC AAE23757;
 XX 10-SEP-2002 (first entry)
 DT Human metabotropic glutamate (mGluR4) receptor protein.
 DE Human metabotropic glutamate receptor; mGluR4; neurodegeneration;
 KW antipsychotic; anticonvulsant; analgesic; antidepressant; antiepileptic.
 XX Homo sapiens.
 OS US6384205-B1.
 PN 07-MAY-2002.
 XX 18-AUG-2000; 2000US-00641318.
 PR 12-MAR-1996; 96US-0013189P.
 PR 12-MAR-1997; 97US-00816178.
 XX (ELIL) LILLY & CO ELI.
 PA Belagaje RM, Wu S;
 PI WPI; 2002-442818/47.
 DR N-PSDB; AAD38024, AAD38025.
 XX New nucleic acid encoding human metabotropic glutamate receptor, useful
 PT -e.g. in screening for specific agonists and antagonists for treating e.g.
 PT neurodegeneration.
 XX Claim 1; Col 9-16; 35pp; English.
 PS The present invention relates to human metabotropic glutamate receptor
 CC (mGluR4) proteins and polynucleotides encoding such proteins. mGluR4
 CC sequences of the invention are useful for treating acute and chronic
 CC neurodegeneration. They are also used as antipsychotic, anticonvulsant,
 CC analgesic, antidepressant and antiepileptic agents. They are also useful for
 CC the diagnosis and/or treatment of conditions associated with an excess or
 CC deficiency of mGluR4. The present sequence is human mGluR4 protein
 XX Sequence 912 AA;
 SQ
 Alignment Scores:
 Pred. No.: 2,81e-209 Length: 912
 Score: 3004.50 Matches: 564
 Percent Similarity: 97.77% Conservative: 6
 Best Local Similarity: 96.74% Mismatches: 12
 Query Match: 90.96% Indels: 1
 DB: 5 Gaps: 1
 US-10-828-332-6 (1-1755) x AAE23757 (1-912)
 QY 7 GGGGTATCATCATCTTTGGCAACGAGGATGACA---TCAGGTTTCGACCGATCTCTCC 63
 DB 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349

QY 64 AGCCCCACGCTGGAGCAACAAACAGGCGCAACATCTCGTTTCCGAGTTCTTGGAGGACAAAC 123
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 DB 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleValLysCysThr 389
 QY 184 AACCCAGAGCGCATCGGCGCAGACTCGGCCTATAGACAGGAGGGGAAGTGCAGTTCTG 243
 DB 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyValGlnPheVal 409
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 QY 364 ATCAGGAACGCAACTTCTCAGGCAATTCGGGGAACCTGTAACTTCAATGAGAACGA 423
 DB 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAlaGly 469
 QY 424 GACGACCGGCGCTACGACATCTACAGTACCAACTCGCGCAATGGCTCGGCCCGAGTAC 483
 DB 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
 QY 484 AAGTTCATCGGCTCGTGACAGACACCTGCACCTCAGATAGAGCGGATGACAGTGGCCA 543
 DB 490 LysValIleGlySerTyrThrAspHisLeuHisLeuArgIleGluArgMetHisTyrPro 509
 QY 544 GGGAGTGGCCAGCAGCTCGCGCTCATCTGCAGTCTGCCCTGCAGCCCGGCGAGCGA 603
 DB 510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAGACTGTGAAGGCGATCGCTTGTGTGGCACTCGAGCCCTGCACCGGGTACCCAG 663
 DB 530 LysLysThrValLysGlyMetProCysCysTyrHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGACCGCTACACCTGTAGACCTGCCCTACGACATCGGCGCCACAGAGAC 723
 DB 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CGCAGAGCTGCAGCCCATCCCATCTCAAGTTGGAGTGGAGCTCGCGCGGCGCGTG 783
 DB 570 ArgThrGlyCysArgProIleProIleLysLeuGluTyrGlySerProThrAlaVal 589
 QY 784 CTGCCCTCTTCTCGCGCTGGGCACTCGCCGACCTGCTTCTCGTGGTGTACGTTT 843
 DB 590 LeuProLeuPheLeuAlaValGlyIleAlaIleAlaThrLeuPheValIleThrPhe 609
 QY 844 GTGGCTTACAAGATACCCCATCGTCAAGGCTCGGCGCGGAACTAGCTACGTCTG 903
 DB 610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
 QY 904 CTGGGCGCATCTTCTGTGTAGCCCACTACTTCTCATGATCGCAGCGCGGACCTG 963
 DB 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
 QY 964 GGGACTGTTCGCTCGCGCGCATCTTCTTAGGCTCGGCATGAGCATCAGCTACCGGCC 1023
 DB 650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaIle 669
 QY 1024 CTGTGACCAAGACCAACCGCATTTACCGCATCTTTTGGACAGGGGAACCGTCTCAGT 1083
 DB 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
 QY 1084 GCCCGCGCTTTCATCAGCCCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCCCTG 1143
 DB 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709

Db 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 QY 304 GCGCGGTAGGACTCTGCGCTCGCATGGAGCCCGTGGATGGCACCAGCTGCTTAAGTAC 363
 Db 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuTyr 449
 QY 364 ATCAGGAAGCTCAACTCTCAGGCATTCGGGGACCCCTGTACCTTCAATGAGACGGA 423
 Db 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 GACGACCGGGCGCTACGACATCTACCACTGCGCAATGGCTCGGCGCGAGTAC 483
 Db 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
 QY 484 AAGGTCAATCGGTCTGGGACAGACCACTGCACTCAGATAGAGCGGATGAGTGGCCA 543
 Db 490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMethIstPPro 509
 QY 544 GGGAGTGGCCAGCAGTCCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCCGGGAGCGA 503
 Db 510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAAGACTGTGAAGGCGATGGCTGCTGCTGCACTGCGAGCCCTGCACCGGTACACAG 663
 Db 530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGCGGTACACCTGTAAAGACCTGCGCCCTACGACATGCGGCCACAGAGAAC 723
 Db 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CGCAGGAGTGCAGAGCCATCCCATCTGCTCAAGTGGAGTGGAGTGGAGTGGCGCGTGG 783
 Db 570 ArgThrGlyCysArgProIleProIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
 QY 784 CTGCGCTCTCTCTGCGCGTGGGCGATCGCGCCAGCTGCTGCTGCTGCTGCTGCTGCT 843
 Db 590 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValIleThrPhe 609
 QY 844 GTGCGCTACAAGCATACCCCGCATCTGTCAGAGGCTCGGCGCGGAACTGAGCTACGTGCTG 903
 Db 610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
 QY 904 CTGCGCGGATCTTTCTGTGTAGCGCACTTCTCTCATGTCATGTCAGAGCGGACCTG 963
 Db 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
 QY 964 GGGACTGTCTGCTCGCGCGCATCTCTAGGCTCGGCGATGAGCATGAGCTACGCGGCC 1023
 Db 650 GlyThrCysSerLeuArgGlyIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
 QY 1024 CTGCTGACCAAGACCAACCGCATTTTACCGCATCTTTGACGAGCGCAACGGTCCGTGCT 1083
 Db 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
 QY 1084 GCGCGCGTTCATCAGCCCGCTGCGAGCTGGCCATCACCTTCATCTCATCTCCCTG 1143
 Db 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
 QY 1144 CAGCTCTCGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1203
 Db 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
 QY 1204 CAGGACCAACGACACTTACCCCGCTTTCAGGGGGCTGCTCAAGTGGCAGCATCTCG 1263
 Db 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
 QY 1264 GACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
 Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
 QY 1324 TAGCGCATCAAGCCGAGCGTGGCGAGCTTCAAGAGCCGACGCTTCAAGAGCCGACGCT 1383
 Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789

QY 1384 ACCATGTACACCACTGCACTTCTGCGTGGCTTCACTCCCATCTTTTGGCACCTCA 1443
 Db 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 809
 QY 1444 CAGTCAGCGGCAAGCTGTACATCCAGCAACACCACTGACCGTCTCCGTGAGTCTGAGC 1503
 Db 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 829
 QY 1504 GCTTCAGTGTCCCTGGGATGCTTACATGCCCAAGTCTACATCATCTCTTCCACCCG 1563
 Db 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
 QY 1564 GAGCAGACGTGCCAAGCGCAGTCTCAAGCGTGGTCAACCGCGCCGCCACCATG 1623
 Db 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 869
 QY 1624 TCCAAACAAGTTCACACAGAGGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG 1683
 Db 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
 QY 1684 TGTGAGAACCTGAGACCCCGCTGCTACCAACAGACCTACGTCACCTACACCAAC 1743
 Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 909
 QY 1744 CATGCCATC 1752
 Db 910 HisAlaIle 912
 RESULT 10
 ID ADE58170 standard; protein; 912 AA.
 XX ADE58170;
 XX 29-JAN-2004 (first entry)
 XX Human Protein Q14833, SEQ ID NO 4041.
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 OS Homo sapiens.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; Q14833.
 XX New composition comprising two or more isolated polypeptides, useful for
 preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence

QY 1684 TGTGAGAACTGGAGACCCAGCGCTGGCTACCAAAACAGACCTACCTACCTACCAAC 1743
 XX |||||
 Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 909
 XX |||||

QY 1744 CATGCCATC 1752
 Db 910 HisAlaIle 912
 XX |||||

RESULT 11

AD58166
 ID 'ADE58166 standard; protein; 912 AA.

XX AC ADE58166;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human Protein Q14833, SEQ ID NO 4037.

XX KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX OS Homo sapiens.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PP 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GHEO) GEN HOSPITAL CORP.
 XX PA (PARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX DR GENBANK; Q14833.

XX PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 XX PS Claim 1; Page; 1017pp; English.
 XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 912 AA;

Alignment Scores:
 Pred. No.: 2,81e-209 Length: 912
 Score: 3004.50 Matches: 564
 Percent Similarity: 97.77% Conservative: 6
 Best Local Similarity: 96.74% Mismatches: 12
 Query Match: 90.96% Indels: 1
 DB: 7 Gaps: 1

US-10-828-332-6 (1-1755) x ADE58166 (1-912)

QY 7 GGGGTATCATCATCTTTGCCAACGAGGATGACA---TCAGGGTTCCAGCGATACTTCTCC 63
 Db 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
 QY 64 AGCCGACGCTGGACAAACACAGGCGCAATCTCGTTTGGCGAGTTCTGGGAGGACAAAC 123
 Db 350 SerArgThrLeuAspAsnArgArgAsnIleTyrPheAlaGluPheTrpGluAspAsn 369
 QY 124 TTCCATTGCAAGTTGAGCGCGCACGCGCTCAAGAGGGAAGCCACATCAAGAGTGCCACC 183
 Db 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysLysCysThr 389
 QY 184 AACCGAGAGCGCATCGCGCAGGACTCGCGCTATGACGAGGAGGAGGAGGAGTGCAGTTCGTG 243
 Db 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyValGlnPheVal 409
 QY 244 ATTGACGCTGTACGCCCATCGGCGCACGCGCTGACGCGCATGACCGCTGACCTGTGTCCTCC 303
 Db 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuLeuCysPro 429
 QY 304 GCGCGGTAGGACTCTGCCCTCGCATGACACCCCGTGGATGGACCCAGCTGCTTAAGTAC 363
 Db 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
 QY 364 ATCAGGAACGTCAACTTCTCAGGCAATTCGGGGAAACCTGTAACTTCAATGAGAACGGA 423
 Db 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 GACGACCGGCGCGCTACGACATCTACAGTACCAACTCGCGCAATGGCTCGCGCCGAGTAC 483
 Db 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
 QY 484 AAGTCACTCGGCTCGTGACACACACCTGCACCTCAGACTCAGANTAGACCGATGCGGCGCA 543
 Db 490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 509
 QY 544 GGGAGTGCCACGACGCTCGCGCTCCATCTGCAGTCTGCCCTGCGCAGCCCGGGGAGGGA 603
 Db 510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAAGACTGTGAAGGGCATGGCTGTGCTGGCATCGAGCCCTGACCGGGTACCGAG 663
 Db 530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACTGCCCTACGACATCGCGGCCACAGAGAAC 723
 Db 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CGCAGAGCTCCAGCGCCATCCCATCTCAAGTTGGAGTGGAGTCCCGCGGCGCGGTG 783
 Db 570 ArgThrGlyCysArgProIleProIleLysLeuGluTrpGlySerProTrpAlaVal 589
 QY 784 CTGCGCCCTCTTCTCGCGCGTGGTGGGATCGCGCCAGCGCTGTTCTGGTGGTCAAGTTT 843
 Db 590 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValIleThrPhe 609
 QY 844 GTGCGCTACAACGATACCCCATCTGTAAGCGCTCGGCGCGGGAACCTAGCTACGTGCTG 903
 XX |||||

Db 610 ValArgTyrAsnAspThrProIleValIysAlaSerGlyArgGluLeuSerTyrValLeu 629
QY 904 CTGGCGGCGATCTTCTGCTGCTACGCCACTCTCTCTCATGATCGCAGACCGGACCTG 963
Db 630 LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 649
QY 964 GGGACCTGTTCTCTCGCGCGATCTCTCTAGGCGCTCGCATGAGCATCAGCTACGCGGCC 1023
Db 650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
QY 1024 CTGCTGACACAGCAACCGCATTTACCGCATCTTTTGGACGGGCAACCGTGGTCACT 1083
Db 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
QY 1084 GCCCGCGCTTCATCAGCCCGCGCTCGCATGCGCATCAGCTTCATCTCATCTCCCTG 1143
Db 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
QY 1144 CAGCTGCTCGGCATCTGCGTGTGGTTCGTGGTGGACCCCTCCACTCGGTGGTGGACTTC 1203
Db 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
QY 1204 CAGGACCAACGACACTTGTACCCCGCTTTGCGAGGGCGTCTCAAGTGGCAGCATCTCG 1263
Db 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
QY 1264 GACCTGCTCCCTCATCTGCTGCTGGCTACAGCATGCTGCTGATGGTCACGTGACTGTG 1323
Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
QY 1324 TACGCCCATCAAGACCCGAGCGCTGCCGAGACCTTCAACGAGGCCCAACCCATCGGCTTC 1383
Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
QY 1384 ACCATGTACACACTGCTGCTGCTGGCTGCTTTCATCCCATCTTTTGGACACTCA 1443
Db 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 809
QY 1444 CAGTCAGCGCAGCAAGCTGTACATCCAGACACACACACACACACACACACACACAC 1503
Db 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerLeuSer 829
QY 1504 GCTTCAGTGTCTCTCGGATGCTGTACATGCCCCAAAGTCTACATCATCTCTTCCACCCG 1563
Db 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
QY 1564 GAGCAGACGTGCCCAAGCGCAGCTCTCAAGCGGTGTCAACGCGCGCCACCATG 1623
Db 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 869
QY 1624 TCCACAAAGTTCACACAGAGGGCACTTCAGGCCCATGGGAGCCCAATCAGAGCTG 1683
Db 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
QY 1684 TGTGAGAACCTGGAGACCCCGCTGGCTGTACCAACAGACCTAGCTCAGCTTACACCAAC 1743
Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 909
QY 1744 CATGCCATC 1752
Db 910 HisAlaIle 912
RESULT 12
ADO29094
ID ADO29094 standard; protein; 912 AA.
XX AC ADO29094;
XX AC ADO29094;
DT 29-JUL-2004 (first entry)
XX Human novel GPCR GRM4, SEQ ID NO:193.
DE Human novel GPCR GRM4, SEQ ID NO:193.
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW

transgenic mouse; neurological disorder; adrenal gland disorder;
colon disorder; intestinal disorder; cardiovascular disorder;
muscular disorder; blood disorder; immune disorder; bone disorder;
joint disorder; metabolic disorder; nutritive disorder; cancer;
kidney disorder; liver disorder; lung disorder; breast disorder;
ovary disorder; uterus disorder; prostate disorder; testis disorder;
skin disorder; stomach disorder; pancreas disorder; spleen disorder;
thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
CNS; central nervous system; respiratory; antiarrhythmic; antidiabetic;
virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;
dermatological; antiulcer; antithyroid; antiallergic; anorectic;
immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
receptor.

Homo sapiens.

WO2004040000-A2.

13-MAY-2004.

09-SEP-2003; 2003WO-US028226.

09-SEP-2002; 2002US-0409303P.

09-APR-2003; 2003US-0461329P.

(PRIM-) PRIMAL INC.

Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

WPI; 2004-390329/36.

N-PSDB; ADO29776.

Novel mammalian G protein coupled receptors, useful for identifying
compounds that modulates diagnosing and treating disease condition
associated with GPCR dysfunction e.g. autoimmune diseases, angina
pectoris, Parkinson's disease.

Claim 1; SEQ ID NO 193; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors
(GPCRs) and nucleic acids encoding them. The invention also relates to
sequences at least 90% identical to the GPCR proteins and nucleic acids
of the invention; methods of treating, preventing or diagnosing diseases
associated with GPCRs of the invention; methods of screening for
compounds useful in the treatment of GPCR-related diseases; a transgenic
mouse comprising a GPCR gene of the invention; a mouse comprising a
mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
from the transgenic mice; kits comprising several mice, each of which has
a mutation in a different GPCR gene of the invention; and kits comprising
probes which hybridise to GPCR polynucleotides of the invention. The
invention further discloses variants of the GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
be used in the diagnosis, treatment or prevention of a wide variety of
diseases including neurological disorders (e.g., Alzheimer's disease,
depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
disorders of the adrenal gland; disorders of the colon or intestine
(e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
myocardial infarction); muscular disorders; blood disorders (e.g.,
anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
obesity, enzyme deficiency-related diseases or vitamin deficiency-related
diseases); and disorders of the kidney, liver, lung, breast, ovary,
uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
thyroid (e.g., cancers). The present sequence represents a GPCR of the
invention. Note: The full sequence data for this patent did not form part
of the printed specification; those sequences not shown were obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 912 AA;
 Alignment Scores:
 Pred. No.: 2,81e-209 Length: 912
 Score: 3004.50 Matches: 564
 Percent Similarity: 97.77% Conservative: 6
 Best Local Similarity: 96.74% Mismatches: 12
 Query Match: 90.96% Indels: 1
 DB: 8 Gaps: 1
 US-10-828-332-6 (1-1755) x ADO29094 (1-912)
 QY 7 GGGGTATCATCTCTTTGCCACGAGATGACA---TCAGGGTTCCAGCATCTCTCC 63
 Db 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
 QY 64 AGCCGACCGCTGACAAACAGCGCAACATCTGGTTTGGCCAGTCTTGGGAGGACAAC 123
 Db 350 SerArgThrLeuAspAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 369
 QY 124 TTCCATTGCAAGTTGAGCCGCCAGCGCTCAAGAGGGAAGCCACATCAAGAGTGCAAC 183
 Db 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysLysCysThr 389
 QY 184 AACCGAGCGCATCGGCGCAGAGCTCGGCTATGAGCAGGAGGAGGTGCAAGTTCGTG 243
 Db 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
 QY 244 ATTGACGCTGTGACGCCATGGCCACGCGCTGCACGCCATGCACCGTCACTGTGTC 303
 Db 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 QY 304 GCGCGGTAGGACTCTGCTCCCTCGCATGAGCCCGCTGGATGGCAGCCAGCTGTCTAAGTAC 363
 Db 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
 QY 364 ATCAGGAAGCTCAATCTTCAGCATTTGGGGAAACCTGTAACTTCAATGAGAACGGA 423
 Db 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 GACGACCGGGCGCTACACATCTACAGTACCACTCGCAATGGCTCGGCCGAGTAC 483
 Db 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
 QY 484 AAGGTCACTCGGTGAGACAGACCACTGCACCTCAGAAATAGAGCGGATGCAAGTGGCCA 543
 Db 490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMethIstTrpPro 509
 QY 544 GGGAGTGGCAGAGCTGCGCGCTCCATCTGCACTGCTCCCTCGCAGCCCGGGAGCGA 603
 Db 510 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAGACTGTAAAGGGATGCTGCTGCTGGCACTGGAGCCCTGCACCGGGTACCG 663
 Db 530 LysLysThrValIleGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGACCGCTACACCTGTAAAGCTGCGCCCTACGACATGCGGCCACAGAGAAC 723
 Db 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CCGCAGAGTGCAGCCCATCCCATCTGTCAGTGTGGAGTGGAGTCTCGCCGGGCGCG 783
 Db 570 ArgThrGlyCysArgProIleProIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
 QY 784 CTGCCCCCTTCTTCTGGCCGTGGTGGCATCGCGCCAGCTGTTCTGTGGTGTCTACGTTT 843
 Db 590 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValIleThrPhe 609
 QY 844 GTGCGCTACAGATACCCCATCTGTCAGAGGCTCGGGCCGGCACTGAGCTACGTGCTG 903
 Db 610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
 QY 904 CTGGCGGGCATCTTTCTGTGTACGCCACTACCTCTCTCATGATCGCAGCGGACCTG 963

Db 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
 QY 964 GGGAGCTGTCTCTCGCGCATCTTCTTAGGCGCTCGGCATGAGCATGAGTACGCGGCC 1023
 Db 650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
 QY 1024 CTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGCAACCGTGGTCACT 1083
 Db 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
 QY 1084 GCCCGCGCTTTCATCAGCCCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCCCTG 1143
 Db 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
 QY 1144 CAGCTGCTCGGCATCTGGCTGTGGTGGTGGAGCCCTCCCATCTCGGTGGTGGACTTC 1203
 Db 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
 QY 1204 CAGGACCAACCGACACTTGAACCCCGCTTTGCCAGGGCGTGTCTCAAGTGCACATCTCG 1263
 Db 730 GlnAspGlnArgThrLeuAspProArgPheAlaAGlyValLeuLysCysAspIleSer 749
 QY 1264 GACCTGTCCCTCATCTGCTGCTGGCTACAGCATGCTGCTGATGGTCACTGCTACTG 1323
 Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
 QY 1324 TACGCGCATCAAGACCCGAGGGGTGCCGAGACTTCAACGAGGCGCAAGCCCATCGCTTC 1383
 Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
 QY 1384 ACCATGTACACCACTGCAATTGTCTGGCTGGCTTCATCCCCCATCTTTTTCGCACCTCA 1443
 Db 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 809
 QY 1444 CAGTCAGCGGACAGCTGTACATCCAGAACCACTGAGCGGTCTCGTGGTCTGAGC 1503
 Db 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 829
 QY 1504 GCTTCAGTGTCTCTGGGATGCTTACATGCTCCCAAGTCTACATCATCTCTTTCACCCG 1563
 Db 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro 849
 QY 1564 GAGCAGAACGTGCCCAAGCGCAGTCTCAAGCGGTGGTCCACCGCCGCCACCATG 1623
 Db 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 869
 QY 1624 TCCAAAGATTTCACAGAGGGGCACTTCAGGCCCAATGGGGAAGCCCAATCAGAGCTG 1683
 Db 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
 QY 1684 TGTGAGAACCCTGGAGACCCCGCTGCTACCAAGACAGCTACCTACCTACACCAAC 1743
 Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
 QY 1744 CATGCCATC 1752
 Db 910 HisAlaIle 912
 RESULT 13
 ADO89114
 ID ADO89114 standard; protein; 912 AA.
 XX ADO89114;
 AC ADO89114;
 XX 21-OCT-2004 (first entry)
 DT Human urological disorder related protein 115 SEQ.66.
 DE urological disorder; uropathic; cytostatic; urinary incontinence;
 KW benign prostatic hyperplasia; human.
 XX Homo sapiens.

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XX WO2004065576-A2.
PN
XX
PN
XX
PD
XX
PF
XX
PF
XX
XX
PR
15-JAN-2003; 2003US-0440318P.
PR
04-FEB-2003; 2003US-0444783P.
PR
27-MAR-2003; 2003US-0457901P.
PR
08-MAY-2003; 2003US-0468775P.
PR
19-MAY-2003; 2003US-0471614P.
PR
16-JUN-2003; 2003US-0478742P.
PR
18-JUL-2003; 2003US-0488529P.
PR
30-JUL-2003; 2003US-0491156P.
PR
02-SEP-2003; 2003US-0499594P.
PR
26-SEP-2003; 2003US-0506332P.
XX
PA
(MILL-) MILLENNIUM PHARM INC.
XX
PI
Karicheti V, Silos-Santiago I, Eliasof SD;
XX
XX
DR
N-PSDB; ADQ89113.
XX
XX
PT
Use of polypeptides related to urological disorders, e.g. 44390, 54181,
PT
211 or for identifying a compound capable of treating a urological
PT
disorder or identifying and treating a subject having a urological
PT
disorder.
XX
XX
PS
Claim 1; SEQ ID NO 66; 542pp; English.
XX
CC
The present invention describes the use of polypeptides related to
CC
urological disorders for identifying a compound capable of treating a
CC
urological disorder, identifying a subject having a urological disorder,
CC
or treating a subject having a urological disorder. Also described: (1) a
CC
method for identifying a compound capable of treating a urological
CC
disorder; (2) a method for identifying a subject having a urological
CC
disorder; and (3) a method for treating a subject having a urological
CC
disorder. The compound has uropathic and cytosolic activities. The
CC
polypeptides related to urological disorders are useful for identifying a
CC
compound capable of treating a urological disorder, identifying a subject
CC
having a urological disorder, or treating a subject having a urological
CC
disorder. Disorders include urinary incontinence and benign prostatic
CC
hyperplasia. The present sequence represents a human urological disorder
CC
related protein, which is used in the exemplification of the present
CC
invention.
XX
XX
SQ
Sequence 912 AA;

Alignment Scores:
Pred. No.: 2,81e-209 Length: 912
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 90.96% Indels: 1
DB: 8 Gaps: 1

US-10-828-332-6 (1-1755) x ADQ89114 (1-912)
OY
7 GGGGTATCATCATCTTTCGCCAAGGAGGATGACA---TCAGGGTTTCGACCGATACTTCTCC 63
DB
330 GlyAlaValThrIleLeuProlyArgMetSerValArgGlyPheAspArgTyrPheSer 349
OY
64 AGCCGACGCTGGACAACACAGGCGCAACATCTGGTTTTCGAGTTCTGGGAGGACAAC 123
DB
350 SerArgThrLeuAspAsnAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 369
OY
124 TTCATTTCAGATTGAGCGGCGCACCGCTCAAGAGGGAAGCCACATCAAGAGTGCACC 183
DB
370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysCysThr 389
OY
184 AACCGAGAGCGCATCGGGCAGGACTCGGCCTATGAGCAGGAGGGGAGGAGTGCAGTTCGTG 243
DB
390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGlnGlnGluGlyLysValGlnPheVal 409
OY
244 ATTGACCGCTGTATGACCATGGCCACCGCTGCACGCCATGACCGCTGCTGTGCC 303
DB
410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
OY
304 GCGCGCTAGGACTCTCCCTCGCATGGACCCCGTGGATGGCACCACCGCTCTTAAGTAC 363
DB
430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
OY
364 ATCAGGAACGTCAACTTCTCAGGCATTGCGGGGAACCTGTAACTTCAATGAGAACGGA 423
DB
450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
OY
424 GACGACCGGGCGCTACGACATCTACAGTACCAACTGCGCATGCTCGCGCAGTAC 483
DB
470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
OY
484 AAGGTATCGGCTCGTGGACAGACCACTGACCATCTCAGAAATAGAGCGGATGCAGTGGCCA 543
DB
490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 509
OY
544 GGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCACTGCTGCCCTGCCAGCCCGGGAGGGA 603
DB
510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
OY
604 AAGNAGACTGTAAGGCGATGGTGTGCTGTCGACCTGCGAGCCCTGACCGGCTACCG 663
DB
530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
OY
664 TACCAGTGGACCGCTACACTGTAAAGACCTGCGCCCTACGACATGCGGCCCCACAGAGAAC 723
DB
550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
OY
724 CGCAGCAGCTGCCACGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGCCGTG 783
DB
570 ArgThrGlyCysArgProIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
OY
784 CTGCCCCCTCTCTGCGCGTGGTGGGATCGCCCGCCAGCTGTTCGTGGTGTGTCACGTTT 843
DB
590 LeuProLeuPheLeuAlaValAlaGlyIleAlaAlaThrLeuPheValIleThrPhe 609
OY
844 GTGGCGTACAAAGATACCCCATCGTCAAGCGCTCGCGCGGGAACCTGAGTACGTGCTG 903
DB
610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
OY
904 CTGCGCGGCGCATCTTTCTGTGCTACGCCACTACCTTCCTCATATGTCGAGAGCCGAGCTG 963
DB
630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
OY
964 GGGACCTGTTGCTCCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGTACGCGGCC 1023
DB
650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
OY
1024 CTGCTGACCAAGACCAACCGCATTTTACCGCATCTTTTTCAGAGGGAACCGCTCGCTCAGT 1083
DB
670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
OY
1084 GCGCGCGGCTTTCATPACGCGCGCTCGCAGCTGCGCATCACCTTCCTCATCTCTCCCTG 1143
DB
690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
OY
1144 CAGTGTCTCGGCTCTCGGTGTGGTTCGTGGTGGACCCCTCCCACTGGTGGTGGACTTC 1203
DB
710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
OY
1204 CAGSACCAACGAGACACTTTCACCCCGCTTTGCCAGGCGCGTCTCAAGTGCAGACTCTCG 1263
DB
730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
OY
1264 GACGTGCTCCCTCATCTCTGCTGCTGGGTACAGCATGCTGTGATGGTGCAGTGTGCTGTG 1323
DB
1323
```

Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
 QY 1324 TAGCCATCAAGACCCGAGCGTCCGAGACCTTCAAGAGGCGCAAGCCCATCGCTTC 1383
 Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
 QY 1384 ACATGTACACACCTGCAATGTCTGGCTGGCTTCATCCCATCTTTTGGCAGCTCA 1443
 Db 790 ThrMetTyrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 809
 QY 1444 CAGTCAGCGCACAAAGCTGTACATCCAGACACACACTGACGCTCTCCGTGAGTCTGAGC 1503
 Db 810 GlnSerAlaAspLysLeuIleGlnThrThrLeuThrValSerValSerLeuSer 829
 QY 1504 GCTTCAGTGTCCCTGGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCACCGC 1563
 Db 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
 QY 1564 GAGCAGAACGTCGCCAAGCGCAAGCGCAGTCTCAAGCGGTGTACCGCGCCGACCATC 1623
 Db 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 869
 QY 1624 TCCAACAAGTTCACACAGAGGCGCACTTCAGSCCAATGGGGAAGCCCAATCAGAGCTG 1683
 Db 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
 QY 1684 TGTGAGAACCTGGAGACCCGAGCTGGCTTACCAACAGACCTTACGTCACCTACACCAAC 1743
 Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
 QY 1744 CATGCCATC 1752
 Db 910 HisAlaIle 912

RESULT 14
 ID AAR72092
 AC AAR72092 standard; protein; 912 AA.
 XX AC AAR72092;
 XX 25-MAR-2003 (revised)
 DT 26-SEP-1995 (first entry)
 XX
 DE Human mGluR4.
 XX
 KW Human metabotropic glutamate receptor subtype 4; mGluR4; hmGluR4;
 KW signal transducer.
 XX
 OS Homo sapiens.
 XX
 PN W09508627-A1.
 XX
 PD 30-MAR-1995.
 XX
 PF 07-SEP-1994; 94WO-EP002991.
 XX
 PR 20-SEP-1993; 93EP-00810663.
 PR 19-AUG-1994; 94GB-00016553.
 XX
 XX (CIBA) CIBA GEIGY AG.
 XX
 XX Flor PJ, Kuhn R, Lindauer K, Puettner I, Knoepfel T;
 XX WPI: 1995-139596/18.
 DR N-PSDB; AAQ89342.
 XX
 XX Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and 7 - also
 PT corresp. DNA and antibodies, useful for identifying cpds. which modulate
 PT signal transduction activity.
 XX
 XX Claim 2; Page 44-48; 110pp; English.
 PS
 XX Human metabotropic glutamate receptor subtype 4 (hmGluR4) cDNA clones
 CC

CC were isolated from a cerebellum cDNA library using a rat mGluR4 probe.
 CC Clone cMR20 lacked the 5' end of the hmGluR4 gene. PCR using human
 CC genomic or brain cDNA as template was used to obtain a complete gene
 CC sequence (given in AAQ89342) encoding hmGluR4 (AAR72092). Recombinant
 CC hmGluR4 was produced in mammalian cells. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX SQ Sequence 912 AA;

Alignment Scores:
 Pred. No.: 4,648-209 Length: 912
 Score: 3001.50 Matches: 563
 Percent Similarity: 97.77% Conservative: 7
 Best Local Similarity: 96.57% Mismatches: 12
 Query Match: 90.87% Indels: 1
 DB: 2 Gaps: 1

US-10-828-332-6 (1-1755) x AAR72092 (1-912)

QY 7 GGGGTATCATCATCTTTGCCAACGAGGATGACA---TCAGGGTTGACCGATCTCTCTCC 63
 Db 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
 QY 64 AGCCCGACGCTGACACAAACAGGCGCAACATCTGTTTGGCGAGTCTCTGGGAGGACAC 123
 Db 350 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 369
 QY 124 TTCCATTGCAAGTTGAGCGCCACCGCTCAAGAGGGAAGCCACATCAAGAGTGCAC 183
 Db 370 PheHisCysLysLeuSerArgHisAlaLeuLysGlySerHisValLysCysThr 389
 QY 184 AACCGAGAGCGCATCGGCGAGGACTCGGCCTATATGACAGAGGGAAGGTGCGATTCTGTG 243
 Db 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
 QY 244 ATTGACGCTGTGTACGCCATGGCCACCGGCTGACGCGCATGACCGTGCCTGTGTCCC 303
 Db 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 QY 304 GCGCGCTAGGACTCTGCGCTCGCATGACCCCGTGGATGGCACCAGCTGCTTAAGTAC 363
 Db 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
 QY 364 ATCAGAACTCACTTCTCAGGCAATGCGGGGAAACCTGTAACTTCAATGAGAACGGA 423
 Db 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 GAGCAGCGGGCGCTACGACATCTACAGTACCACTCGCGCAATGGCTCGGCGCGAGTAC 483
 Db 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
 QY 484 AAGGTCATCGGCTCGTGACAGACACCTGACACCTCAGAATAGAGCGGATGCAGTGGCCA 543
 Db 490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 509
 QY 544 GGGAGTGGCCAGCAGCTCGCGCTCCATCTGCACTCTGCGCTGCGCAGCCGCGGAGCGA 603
 Db 510 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAAGACTGTGAAGGGCATGGCTTGTCTGGCACTGGGAGCCCTGCAACCGGGTACCGAG 663
 Db 530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACCTGCGCCCTACGACATCGGCGCCACAGAGAAC 723
 Db 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CGCAGAGCTGCACGCCCATCCCCATCGTCAAGTTGGAGTGGGACTCGCGCGGCGCGT 783
 Db 570 ArgThrGlyCysArgProIleProIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
 QY 784 CTGCCCCCTTCTCTCGCGCTGGTGGCATGCGCCGACGCTTCTCGTGGTGTCTACGTTT 843

QY	124	TTCCATTGCCAAGTTGAGCCGCCACCGCGCTCAAGAAAGGGAAGCCACATCATCAAGAAGTGCACC	183
DB	62	PhEhIsCySbYsLeuSerArGhIsAlaLeuIySbYsGlySerHIsVaIyLeuIySbCySthr	81
QY	184	AACCGAGAGCCCATCGGCGAGACTTCGGCCCTATGAGCAGGAGGGAAGGTGCAGTTCGTG	243
DB	82	AsnArgGluAArgIleGlyLnAspSerAlaTyrgluGlnGluGlyLySbValGlnPheVal	101
QY	244	ATTGACGCTGTGTACGCCATGGGCCACCGCTGCACGCCCATGCACCGTGCAGCTGTGTGCC	303
DB	102	IleAspAlaValTyrgAlaMetGlyHIsAlaLeuHIsAlaMetHIsArgAspLeuCySbPro	121
QY	304	GGCGCGTAGACTTCGCCCTCGCATGATGACACCCCGTGGATGSCACCCAGCTGCTTAAGTAC	363
DB	122	GlyArgValGlyLeuCySbProArgMetAspProValAspGlyThrGlnLeuLeuIySbTy	141
QY	364	ATCAGGAACGTCAACTCTCAGGCATTCCGGGGAAACCTGTAACTTCAATAGAGAACGGA	423
DB	142	IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly	161
QY	424	GACGACCGGGCGCTACGACATCTACCACTACCACTGCCAATGGCTCGGCCGAGTAC	483
DB	162	AspAlaProGlyArgTyrgAspIleTyrglnTyrglnLeuArgAsnAspSerAlaGlnTyrg	181
QY	484	AAAGTCATCGGCTCGTGACAGACCACTGCACCTCAGAAATAGACGGCATCGATGCGCA	543
DB	182	LySValIleGlySerTrpThrAspHIsLeuHIsLeuArgIleGluArgMetHIsTrpPro	201
QY	544	GGGAGTGGCCAGACAGTCCCGCGCTCCATCTGCAGTCTGCCCTGCAGCCCGGGAGCGA	603
DB	202	GlySerGlyGlnGlnLeuProArgSerIleCySbSerLeuProCySbGlnProGlyGluArg	221
QY	604	AAGAAGACTGTGAAGGGCATGGCTTGTGTGGCACTGCGAGCCCTGCACCGGTACCAAG	663
DB	222	LySlySbThrValLySbGlyMetProCySbCySbTrpHIsCySbGluProCySbThrGlyTyrgln	241
QY	664	TACCAAGTGGACCGCTACACCTGTAAAGACTGCCCTACGACATGGCGGCCACAGAGAAC	723
DB	242	TyrglnValAspArgTyrgThrCySblySbThrCySbProTyrgAspMetArgProThrGluAsn	261
QY	724	CGCACGAGCTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGCGCGTG	783
DB	262	ArgThrGlyCySbArgProIleProIleIleLySbLeuGlnTyrglySerProTrpAlaVal	281
QY	784	CTGCCCTCTTCTGTGGCGGTGGGCATCGCCGCCACGCTGTGTGGTGGGTCAAGTTT	843
DB	282	LeuProLeuPheLeuAlaValAlaGlyIleAlaAlaThrLeuPheValIleThrPhe	301
QY	844	GTGCGCTACACGATACCCCATCGTCAAGCCCTCGGCGCGGGAACGTAGCTAGCTGCTG	903
DB	302	ValArgTyrgAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrgValLeu	321
QY	904	CTGCGCGGCATCTTCTGTGTACGCCCATCTCTCTCATGATCGAGAGCCGCGACCTG	963
DB	322	LeuAlaGlyIlePheLeuCySbTyrgAlaThrThrPheLeuMetIleAlaGluProAspLeu	341
QY	964	GGGACCTGTTCGTTCGCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGCTACGCGGCC	1023
DB	342	GlyThrCySbSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrgAlaAla	361
QY	1024	CTGCTGACCAAGACCAACCGCATTTACGCATCTTTCAGCAGGCGCAACCGTCCGTGAGT	1083
DB	362	LeuLeuThrLySbThrAsnArgIleTyrgIlePheGluGlnGlyLySbArgSerValSer	381
QY	1084	GCCCGCGGTTTTTCATCAGCCCGCGCTCGCAGCTGGCCCATCACTTTCATCTCATCTCCGCTG	1143
DB	382	AlaProArgPheIleSerProValSerGlnLeuAlaIleThrPheSerLeuIleSerLeu	401
QY	1144	CAGCTGCTCGGCATCTCGGTGTGTTGTGTGTGGACCCCTCCCACTCGGTGGTGCATTC	1203
DB	402	GlnLeuLeuGlyIleCySbValTrpPheValValAspProSerHIsSerValLeuAspPhe	421

QY	1204	CAGACCAACGGACACTTGATCCCGCGTGTTCGACGGGGCGTGCTCAAGTCGGACACTCTCG	1263
Db	422	GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer	441
QY	1264	GACCTGTCCCTCATCTCCCTGCTGGGCTCAGACATGCTGCTGATGCTGTCAGTGTACTGTG	1323
Db	442	AspLeuSerLeuIleLysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal	461
QY	1324	TACGCCATCAAGACCCGAGGCGTGCCTGGAGACCTTCAACGAGGCGCAAGCCCATCGCGTTC	1383
Db	462	TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe	481
QY	1384	ACCATGTACACCACTGCATGTCTGCTGGCTTCATCCCACTCTTTTWTGGCACTCA	1443
Db	482	ThrMetTyrThrThrCysIleValTyrLeuAlaPheIleProIlePhePheGlyThrSer	501
QY	1444	CAGTCAGCGCAACGCTGTACATCCAGAACCAACCACTGACGGTCTCCGTGAGTCTTGAGC	1503
Db	502	GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer	521
QY	1504	GCTTCAGTGTCCCTGGGGAGCTCTACATGCCCAAGTCTACATCATCTCTTCCACCCG	1563
Db	522	AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro	541
QY	1564	GAGCAGAACTGCGCCAAAGCCGAGTCTCAAAGCCGTGTGCTACCGCGCGCCACCATG	1623
Db	542	GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet	561
QY	1624	TCCAAACAAGTTCACACAGAAGGGCAACTTCAGCGCCCAATGGGGAAGCCAAATCAGAGCTG	1683
Db	562	SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu	581
QY	1684	TGTGAAACCTGGAGACCCCA	1704
Db	582	CysGluAsnLeuGluAlaPro	588

Search completed: June 17, 2005, 18:40:29
Job time : 307 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 04:06:08 ; Search time 5983 Seconds
(without alignments)
11165.434 Million cell updates/sec

Title: US-10-828-332-6
Perfect score: 1755
Sequence: 1 atgcacgggtatcatcatc.....acacacacatgccatctag 1755

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gseq1:*
9: gb_gseq2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	841.4	47.9	3675	3 AK038395	AK038395 Mus muscu
2	841.4	47.9	3693	3 BC051384	BC051384 Mus muscu
3	823.2	46.9	2748	9 AY401210	AY401210 Mus muscu
4	822.6	46.9	3399	3 BC034118	BC034118 Mus muscu
5	807.2	46.0	2748	9 AY401208	AY401208 Homo sapi
6	806.2	45.9	2667	9 AY406145	AY406145 Mus muscu
7	801.4	45.6	2671	9 AY406143	AY406143 Homo sapi
8	793.8	45.2	4209	3 AK053447	AK053447 Mus muscu
9	788.2	44.9	2611	9 AY401209	AY401209 Pan trogl
10	777.4	44.3	2671	9 AY406144	AY406144 Pan trogl
11	708	40.3	782	6 CD353576	CD353576 UI-M-GMO-
12	579	33.0	711	7 CN409312	CN409312 170004243
13	531.2	30.3	653	1 AU296039	AU296039 AU296039
14	503	28.7	1484	3 CR717163	CR717163 Tetraodon
15	497.8	28.3	582	5 BP359939	BP359939 BP359939
16	477.8	27.2	1051	9 CN5047PP	CN5047PP Tetraodon
17	449.8	25.6	787	4 BT732193	BT732193 603352796
18	440.6	25.1	608	4 BM490671	BM490671 ppp2n.pk0
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21	385	21.9	795	7 CN460548	CN460548 UI-M-HB0-
22	380	21.7	702	7 CK314839	CK314839 SB0204082
23	368.6	21.0	772	5 BX873944	BX873944 BX873944
24	367	20.9	679	5 BM964289	BM964289 UI-M-EQ0-

25	350.8	20.0	723	6 CA344834	CA344834 675311 NC
26	346	19.7	973	4 B1827857	B1827857 603074065
27	344.8	19.6	732	6 CD609655	CD609655 56040124H
28	341.8	19.5	941	2 BE779818	BE779818 601465317
29	340.8	19.4	872	9 CNS02JYV	AL200851 Tetraodon
30	334.4	19.1	895	4 BG261524	BG261524 602373277
31	328.6	18.7	808	5 BU292395	BU292395 603604634
32	324	18.5	839	9 CNS028BY	AL185767 Tetraodon
33	322.2	18.4	1078	9 CNS054KQ	AL320867 Tetraodon
34	316.6	18.0	777	5 BU456417	BU456417 603217533
35	315.2	18.0	943	9 CNS058KW	AL326057 Tetraodon
36	312.6	17.8	666	9 CE724887	CE724887 tigr-gss-
37	311.2	17.7	373	2 BE207131	BE207131 ball609.y
38	303.6	17.3	907	9 CNS04HBU	AL290739 Tetraodon
39	302.2	17.2	2182	3 AK034263	AK034263 Mus muscu
40	301.6	17.2	554	4 BM681239	BM681239 UI-B-EJ0-
41	294.4	16.8	521	7 CN468842	CN468842 hh Ab Bra
42	290.4	16.5	633	6 CB517356	CB517356 seal1gbb53
43	285.6	16.3	600	4 BG806878	BG806878 2042-42 M
44	284.8	16.2	2007	3 BC022720	BC022720 Mus muscu
45	283	16.1	754	6 CD609656	CD609656 56040124J

ALIGNMENTS

RESULT 1	AK038395	AK038395	3675 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK038395	Mus musculus adult male hypothalamus cDNA, RIKEN full-length				
DEFINITION	AK038395	RECEPTOR 8 PRECURSOR, full insert product.				
ACCESSION	AK038395	AK038395.1	GI:26086504			
VERSION	AK038395	HTC; CAP trapper.				
KEYWORDS	AK038395	Mus musculus (house mouse)				
SOURCE	AK038395	Mus musculus				
ORGANISM	AK038395	Mus musculus				
REFERENCE	AK038395	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	AK038395	Carninci, P. and Hayashizaki, Y.				
TITLE	AK038395	High-efficiency full-length cDNA cloning				
JOURNAL	AK038395	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	AK038395	99279253				
PUBMED	AK038395	10349636				
REFERENCE	AK038395	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)				
AUTHORS	AK038395	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	AK038395	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	AK038395	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	AK038395	20530913				
PUBMED	AK038395	11076861				
REFERENCE	AK038395	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)				
AUTHORS	AK038395	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	AK038395	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	AK038395	Nature 409, 685-690 (2001)				
REFERENCE	AK038395	The FANTOM Consortium and the RIKEN Genome Exploration Research				

TITLE
JOURNAL
REFERENCE
AUTHORS

Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3675)

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Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://phantom.gsc.riken.jp/.

FEATURES
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(SWISSPROT|P47743, evidence: FASTA, 97.2%ID, 100%length,
match=2780)"

Query Match 47.9%; Score 841.4; DB 3; Length 3675;
Best Local Similarity 69.6%; Pred. No. 2e-184;
Matches 1155; Conservative 0; Mismatches 501; Indels 3; Gaps 1;

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DB 1444 GGGTTGACCGGATCTTCAGCGCGAGCTGGACACACAGCGCAACATCTGGTTT 1503

QY 103 GCCAGAGTTCTGGAGGACAACTTCCATTTGCAAGTTGAGCGCGCCAGCGCTCAAGAGGGA 162
DB 1504 GCAGAAATTTGGAGAGGAAATTTGGATGCAAAATAGGATCACATGGG--AAGAGGAAC 1560

QY 163 AGCCACATCAAGAAAGTGCACCAACCGAGAGCGCATCGGGAGGAGCTCGGCCTATGAGCAG 222
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QY 223 GAGGGAGAGTTCAGTTCTGTTAGTACCTGTGTACCGATCGGCGCCAGCGCTGCAGCC 282
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QY 283 ATGACACCGTGACTGTGTCGCGCGCGCTAGGAGCTCTGCCCTCGCATGGACCCCGTGAT 342

DB 1681 ATGCACAAGAACTCTGCCCTGGTTTACATAGGCCTTTTCCCAAGGATGGTTACCATCGAT 1740

QY 343 GGACCCAGCTGCTTAACTACATCAGGAACGTCAACTTCTCAGGCATTTGGGGGAAACCT 402

DB 1741 GGGAAAGAGCTACTGGGTTACATCAGGCGCGTGAATTTTAAATGGCAGCGCTGGTACACCT 1800

QY 403 GTAACTTCAATGAAACGAGGAGCGCACCGGGCGCTACGACATCTACCAAGTACCAACTG 462

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BC051384 3693 bp mRNA linear HTC 19-NOV-2003
 Mus musculus glutamate receptor, metabotropic 8, mRNA (cDNA clone
 IMAGE:6466902), containing frame-shift errors.
 BC051384
 BC051384.1 GI:30410848
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 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3693)

Klausner, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Strausberg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
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 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 2338257
 12477932

2 (bases 1 to 3693)
 Strausberg, R.
 Direct Submission
 Submitted (25-APR-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://mgi.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)

Gaithersburg, Maryland;
 Web site: <http://www.nslc.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McLooney, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
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 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 100 Row: j Column: 8
 This clone was selected for full length sequencing because it
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 This clone has the following problem: frame shifted.

FEATURES
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ORIGIN

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 Qy 583 CCCTGCCAGCCCGGGAGCGAAGAGACTGTGAGGCGATGGTTGCTGCTGGCAGCTGC 642
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QY 643 GAGCCCTCAGCCGGGTACAGTACCAAGTGGACGCTACACCTGTAAAGACCTGCCCTTAC 702
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QY 1423 CCCATCTTTTGGCACTCAAGTCAGCGACAGCTGTATCATCCAGACAACACACATG 1482
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QY 1483 ACGGTCTCCGTGAGTCTGAGCGCTTCAGTGCTCCCTGGGGATGCTCTCATGCCCAAGTC 1542
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LOCUS Mus musculus GRM7 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY401210
VERSION AY401210.1 GI:39757199
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2748)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2748)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>2748
/gene="GRM7"
/locus_tag="HCM0814"
gene
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Best Local Similarity 67.9%; Pred. No. 3.2e-180;
Matches 1165; Conservative 0; Mismatches 548; Indels 3; Gaps 1;
QY 42 AGGTTTCACGATATCTTCTCCAGCCGACGCTGGACAAACAGGGCGCAACATCTGGTT 101
Db 1032 AGGATTTTGATGCTTACTTCAATCCCGACACTTTGAAAAACAAACAGAGAAATGTATGGTT 1091
QY 102 TGCCGAGTTCTGGGAGGACAACTTCCATTCGAAGTTGAGCGCCACGCGCTCAAGAGAGG 161
Db 1092 TGCCGAATACTGGGAAGAAACTTCAACTGCAAGTTTGACAAATTAGTGATCCAAAAAGA 1151
QY 162 AAGCCACATCAAGAAGTGCACCAACCGAGAGCGCATCGGCGAGGACTCGGCTTATGACA 221
Db 1152 AGACACGGATCGCAATATGCACAGGACAGAGCGAATTGGAAAAAGCTCTAATTATGACA 1211
QY 222 GGAGGGAAAGGTGAGTTGATTTGATGACGCTGTGTATGCCCATGGGCCACGCGCTGCAAGC 281
Db 1212 GGAGGGTAAAGTACAGATTTTGTGATCGATGCTGTCTATGCCATGGCACATGCCCTTCATCA 1271
QY 282 CATCACCGTACCTGTGTCGCCCGCGTAGGACTCTGCCCTCGCATGGACCCCGTGA 341
Db 1272 CATGAATAAGATCTGTGTGCTGACTACCGGGAGTGTGCCCAGAAATGGAGCAAGCAGG 1331
QY 342 TGGCACCAGCTGCTTAAGTACATCAGGAAAGCTCAACTTCTCAGGCAATTCGGGAAACCC 401
Db 1332 GGGCAAGAGTTGTTGAAGTATATCCGCAATGTTAACTTCAATGTTAGTGTGGAAACCCC 1391
QY 402 TGTAACTTCAATCAGAACCGGACGCAACCGGGCGGCTACGACATCTACCAAGTACCA--- 458
Db 1392 AGTGATGTTTAAACAAAAATGGTGTGATGCTCCAGGACGATATGACATCTTCCAGTACCAAGAC 1451
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BC034118 3399 bp mRNA linear HTC 19-NOV-2003
Mus musculus glutamate receptor, metabotropic 6, mRNA (cdna clone
IMAGE:4511841), containing frame-shift errors.

ACCESSION BC034118
VERSION BC034118.1 GI:21706621
KEYWORDS HTC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 3399)

AUTHORS Klausner, R.D., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Strausberg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Leach, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Schett, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abrams, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Faney, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalek, U., Smal, D.E.,
Schmerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE 22388257

PUBMED 1247932

REFERENCE 2 (bases 1 to 3399)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
Email: cgapbs@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 44 Row: i Column: 22
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
 This clone has the following problem: frame shifted.

FEATURES

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ORIGIN

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Matches 1121; Conservative 0; Mismatches 467; Indels 9; Gaps 1;

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QY 103 GCGGAGTTCTGGAGGACAACTTCATTCGAAGTTGAGCCGCGCAGCGCTCAAGAGGGA 162
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QY 163 AGCCACATCAGAAGTGCACCAACCGAGAGCGCATCGGGCAGGACTCGGCTATGAGCAG 222
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QY 223 GAGGGAAGTGCAGTTCTGATGACGCTGTGTACGCCATGGGCCAGCGCTGCACGCC 282
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QY 463 CGCAATG-----GCTCGCGCGAGTACAAAGTTCATCGGCTGTGTGACACAGCACTG 513
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DB 641 AGACTGGATATGGAAGCTCTCAGTGGTTCAGGCGGACCCCATGAGTGGCCCTTCTCAA 700
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DB 701 TGCAGCTTCCCTGTGGGCTGTGTGAACGGAAGAGATGGTGAAGGGTGTGCCCTGCTGT 760
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QY 1534 CCCAAAGTCTACATCATCTCTTCCACCGGAGCAGAACGTCGCCCAAGCGCAAGCGCAGT 1593
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DB 1721 CTCAAGAGACCTCCACGATGGCGGCCCGCCCAAGA 1757

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RESULT 5

AV401208
 LOCUS
 DEFINITION Homo sapiens GRM7 gene, VIRTUAL TRANSCRIPT, partial sequence,
 Genomic survey sequence.
 ACCESSION AV401208
 VERSION AV401208.1 GI:39757197
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2748)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,

RESULT 6	AY406145	2667 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	Mus musculus GRM8 gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	AY406145 genomic survey sequence.				
ACCESSION	AY406145				
VERSION	AY406145.1 GI:39762119				
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2667)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
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ORIGIN	Query Match 45.9%; Score 806.2; DB 9; Length 2667;				
	Best Local Similarity 69.2%; Pred. No. 2.8e-176;				
	Matches 1148; Conservative 0; Mismatches 498; Indels 13; Gaps 3;				
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Qy	163	AGCCACATCAGAGTGCACCAACCGAGAGCGCATCGGGCAGGACTCGGCTATGAGCAG	222		
Db	1135	AGTCATATAAGAAATGACAGGGCTGGAGCGAATTTGCACGGGATTCATCTTAGAACAA	1194		
Qy	223	GAGGGGAAGTTGACGTTGATGACGCTGTGTACGCGCATGGGCGCAGCGCTGCACGCC	282		
Db	1195	GAAGGAAGTTTCATTTGTAATTTGATGATGATGATTTCCATGGCTTATGCACTGCACAA	1254		
Qy	283	ATGCAACCGTACCTGTGTCCGCGCGCTAGAGACTCTGCGCTCGCATGGACCCCGTGGAT	342		
Db	1255	ATGCACAAAGAACTCTGCGCTGGTTTACATAGGCGCTTTGCCCAAGGATGGTTACCATCGAT	1314		
Qy	343	GGCACCAGCTGCTTAAGTATCATCAGGAACGTCACATTTCTCAGGCATTTGCGGGACCCCT	402		
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Qy	403	GTAACCTTTCAATGAGAACGGAGACCGACCGGGCGCTACGACATCTACCACTGACCAACTG	462		
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Db	1375	GTCACTTTTAATGAGAAATGGAGATGCTCCGGGACGCTACGATATCTTTCCAATATCAGATA	1434		
Qy	463	CGCAATGGCTCGGCCGAGTACAAAGTTCATCGGCTCGTGGACAGACCACTCGACCTCAGA	522		
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Qy	763	TGGGACTCGCGGTGGGCGGTGCTGCCCTCTTCTGCGCGGTGGTGGGATCGCCGCCACG	822		
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Qy	823	CTGTTCTGCTGGTGCACGTTTGTGCGCTACAACGATACCCCATCTGTCAGGGCTCGGGC	882		
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Qy	883	CGGGAATCTGAGCTACGCTGCTGGCGGGCATCTTTCTGTGTACGGCATCTACCTTCTCTC	942		
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Qy	943	ATGATCGCAGAGCGGACCTGGGGACCTGTTCGCTCCGCGCATCTTCTTAGGGCTCGGC	1002		
Db	1909	ATGATTCGGGCACCTGACACAAATCATCTGCTCTTTCCGAAGGATCTTCTCTGGGACTTGT	1968		
Qy	1003	ATGAGCATCAGCTACGCGGCGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGAG	1062		
Db	1969	ATGTGTTTCAGCTATGAGACATTTTGACCAAAACAAACCGATTCACCGGATTAATCGAG	2028		
Qy	1063	CAGGGCAAAACGGTCCGTCAGTCCCGCTTTCATCAGCCCGGCTCGCAGCTGGCCATC	1122		
Db	2029	CAAGGGAAGAAATCTGTACAGCACCTTAAGTTTCATCAGCCAGCATCCAGCTGGTGATC	2088		
Qy	1123	ACCTTCATCTCATCTCCCTGCGAGCTGCTGGCATCTGCGTGTGGTTCGTGGTGGACCCC	1182		
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Db	2149	CCCCACACCATCATTTGATGATGAGAAACAGGAAACATGGATCCCGAAGACCGCAGGGGA	2208		
Qy	1243	GTGCTCAAGTCCGACATCTCGGACCTGTCCCTCATCTGCTGCTGGGCTACAGCATGCTG	1302		
Db	2209	GTGCTCAAGTGTGACATTTCCGATCTGTCACTCATTTGTTTCACTGGGATACAGTATCCTC	2268		
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Db	2269	CTGATGTGTCACTTGTATCTGTTTATGCCATTTAAACACAGAGGGGTTCAGAAACCTTCAAT	2328		
Qy	1363	GAGCCCAAGCCCATCGGCTTCCACCATGTACACCACTGCAATGTTCTGGCTGGCTTTCATC	1422		
Db	2329	GAAGCCAAACCTATTTGATTTTACCATGTACACCACTGCAATTTGTTAGCTTTTCAAT	2388		
Qy	1423	CCCATCTTTTGGCAGCTTCAAGTCCAGCGCAAGCTGTACATCCAGACAAACACACTG	1482		
Db	2389	CCCATCTTTTGGTACAGCCAGCTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2444		
Qy	1483	ACGCTCTCGGTGAGTGTGAGCGTTTCAAGTGTCCCTGGGGATGCTCTACATGCCCAAGTC	1542		
Db	2445	ACTGTCTCCATGAGTTTAAAGTGTCTTCAAGTGTCTCTGGGAATGCTCTATATGCCCAAGTT	2504		

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RESULT 7
 Locus AY406143 2671 bp DNA linear GSS 15-DBC-2003
 DEFINITION Homo sapiens GRM8 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION AY406143
 VERSION AY406143.1 GI:39762117
 KEYWORDS GSS.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2671)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302

REFERENCE 2 (bases 1 to 2671)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.

TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
 Location/Qualifiers
 source 1..2671
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 gene <1..>2671
 /gene="GRM8"
 /locus_tag="HCM2459"

ORIGIN
 Query Match 45.6%; Score 801; DB 9; Length 2671;
 Best Local Similarity 68.5%; Pred. No. 4.6e-175;
 Matches 1136; Conservative 0; Mismatches 514; Indels 9; Gaps 2;

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QY 103 GCGGAGTTCTGGAGGACAACTTCCATTGCAAGTTTGAGCGGCCACCGCTCAAGAAGGA 162
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 Db 1078 GCAGAAATCTGGAGAGAGAAATTTGGCTGCAAGTTAGATCAATGGG---AAAAGAAC 1134
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QY 163 AGCCACATCAAGAAGTGCACCAACGAGAGCGCATCGGCGAGGACTCGGCGCTATGAGCAG 222
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 Db 1135 AGTCATATAAAGAAATGCACAGGGCTGGAGCGAAATGTTCGGGATTCATCTTATGAACAG 1194
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QY 223 GAGGGAAGGTGTCAGTTGCTGATGACGCTGTGTAGCGCTGTGTAGCGGCGCCACGCGCTGACGCC 282
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Db 1195 GAAGAAAGGTCCAATTTGTATTTGATGCTGTATATTCCATGGCTTACGCCCTTGACAAAT 1254
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 QY 283 ATGCACGTGACCTGTGTCGGCGCGGTAGAGACTGTGCCCTCGCATGAGACCCCGGTGGAT 342
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 Db 1255 ATGCACAAAGATCTCTGCCCTGGATACATTTGGCTTTGTCCACGAATAGTACCAATGAT 1314
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 QY 343 GGCACCCAGCTGCTTAAGTACATCAGGAACGTCAACTTCTCAGGCAATTCGCGGGAACCT 402
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 Db 1315 GGGAAAGAGCTACTTTGGTTATATTTCGGGCTGTAAATTTTAAATGGCAGTGTCTGGCACTCCT 1374
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 QY 403 GTAACCTTTCAATGAGAACGGAGACGCACCGGGGGCGCTACGACATCTTACCAGTACCAACTG 462
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 QY 463 CGCAATGGCTCGGCGCGAGTACAAGGTTCATCGGCTCGTGGACAGACCACTGCACTCAGA 522
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 Db 1669 GATCAGAGACCAACATGAACCGCACAGGCTGCCAGCTTATCCCCCATCATCAAAATGGAG 1728
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 QY 823 CTGTTCTGCTGGTGCACGCTTTGTGGCTTACAACGATACCCCATCGTCAAGGCTCGGAC 882
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 Db 1789 ACCTTTGTGATCGTGCACCTTTGTCCGCTATAATGACACACCTATCTGTGAGGGCTTCAGGA 1848
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 Db 1849 CGCGAACTTAGTACGTGCTCTTAACGGGGATTTTTTCTCTGTATTCAATCACGTTTTTA 1908
 |||||
 QY 943 ATGATCGCAGAGCGGACCTGCGGACCTGTTGGCTCCGCGCATCTTCTTAGGGCTCGGC 1002
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 Db 1909 ATGATTCGAGCACCAGATACAATCATATGCTCTTCCGACGGGTCTTCTTAGGACTTGGC 1968
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 QY 1003 ATGAGCATCAGCTACGCGGCGCTGTGTACCAAGACCAACCGCATTTACCGCATCTTTGAG 1062
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 Db 1969 ATGTGTTTCACTATGACGCCCTTCTGACCAAAACAAACCGTATCCACCGAATATTGAG 2028
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 QY 1063 CAGGGAACCGGTGCTGTCAGTGCCTGCGGCTTTTCATCAGCCGCGCTTCGAGCTGCGCATC 1122
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 Db 2029 CAGGGAAGAAATCTGTCAAGCGCCCAAGTTCAATTAGTCCAGCATCTCAGCTGTGTATC 2088
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 QY 1123 ACCTTATCTTCATCTCCCTGACGTGCTCGGCATCTCGGTGTGGTGTGTTGTTGGTGGACCC 1182
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 Db 2269 TTGATGGTCACTGTGACTGTTTATGCCCATAAAGAGAGGTGTGCCAGAGACTTTTCAAT 2328
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QY	162	AAGCCACATCAAGAAAGTGCACCAACCGAGAGCGGCATCGGGCAGGACTCGGGCTATGAGCA	221
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QY	222	GGAGGGGAAGGTGCAGTTTCGTGATTGACGCTGTGTAGCCCATGGCCACGCGCTGCACGC	281
DB	1534	GGAGGGTAAGTACAGTTTGTGATCGATGCTGTCTATGCCCATGGACATGCCCCCTTCATCA	1593
QY	282	CATGCACCGTGCATCTGTGTCCGGCCGGTGAAGACTCTGCGCCTCGCATTGGACCCCGTGG	341
DB	1594	CATGAATAAGGATCTGTGTGCTGACTACCGGGGAGTGTGCCGAGAAATGGACGAAGCAGG	1653
QY	342	TGGCACCCAGCTGCTTAAGTATACATCAGGAACGTCAACTTCTCAGGCATTTGGGGGAACCC	401
DB	1654	GGGCAAGAAGTGTGTGAAGTATATCCGCAATGTGTTAACTTCAATGGTATGCTGGAAACCCC	1713
QY	402	TGTTAACTTCAATGAGAACCGAGACGCAACCGGGCGCTACGACATCTACCAGTACCA--	458
DB	1714	AGTGATGTTTAAACAAAATGTTGATGCTCCAGGAGGATATGACATCTTCAGTACCAGAC	1773
QY	459	ACTGCGCAATGGCTCGGCCGAGTACAAAGGTCAATCGGCTCGTGGACAGACCAACTTGCACTT	518
DB	1774	AACAAACACTACCAATCTCGTTTATCGTCTCATTTGGGAGTGGACAGATGAATGCAGCT	1833
QY	519	CAGAAATAGAGCGGATGCAATGGCCAGGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAG	578
DB	1834	CAATATAGAGGACATGCAATGAGTGGGGCAAGGAGTCCGGGAGATCCACCCCTCTGTGTGCAC	1893
QY	579	TCTGCCCTCCAGCCCGGGGAGCGAAAGAAAGACTGTGAAGGGCATGGTGTCTGCTCGGCA	638
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QY	639	CTGCGAGCCTTGCAACCGGGTACAGTACCAAGTGGACCGGTACACCTGTGAAGACTCGCC	698
DB	1954	TTGTGAGCCCTGTGATGATACCAGTATCAATTTGATGAGATGACATGTCAAGATTGTCC	2013
QY	699	CTACGACATGGCGGCCACAGAGAACCGACGAGCTGGCAGCCCATCCCATCGTCAAGTT	758
DB	2014	CTATGAC--CHAGGCCCAATGAGAACCCGAACCTGGCTGTGAGAAACATCCCAATCATCAAACT	2071
QY	759	GGAGTGGGACTCGCGGTGGGCGGTGCTGCCCTCTTCTCGGCCGTGTGGGCATCGCGCG	818
DB	2072	GGAGTGGCACTCCCTCGGTGGTGAATTCCTGTCTTCTTGGCAATGTGGGATCATTTGC	2131
QY	819	CACGCTGTGTGTGTGTCAGTTTGTGGCTACAAAGTACCCCAATCGTCAAGGCTC	878
DB	2132	CACCATCTTTGTCTATGCGCAACTTCATCCGCTACAATGATACCCATCGTCAGGGCATC	2191
QY	879	GGGCGGGGAATGAGCTACGTGCTGTGGGGGATCTTTCTGTGCTACGCCATACCTT	938
DB	2192	TGGGCGGGAATCAGCTATGTTTATTGAAGGCAATCTTCTCTGCTATATCATCATCCTT	2251
QY	939	CCTCATGATCGCAGAGCGGACCTTGGGGACCTGTTTCGCTCGCGCGCATCTTCTTAGGGCT	998
DB	2252	CCTAATGATTGCCAAGCAGATGTGGCAGTGTGTTCTTCCGAGCTGTCTTCTTGGGGTT	2311
QY	999	CGGCATGAGCATCAGTATCGGGGCCCTGTGTGACCAAGACCAACCGCATTTACCGCATCTT	1058
DB	2312	GGGTATGTGTTATGATTTATGACAGCCCTTTTAAACAAAACCAATCGGATTTTATCGCATAT	2371
QY	1059	TGACACGGGCAAAACGTTGGTGCAGTCCCGGTTTTCATCAGCCCGCGCTCGCAGCTGGC	1118
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QY	1119	CATCACCTTCATCTCTCCCTGCACTGCTCGGCATCTGCGTGTGGTTTCGTGGTGGGA	1178
DB	2432	AATTACCTCCAGTTTAAATATCGGTGCAACTTCTTAGGTGTCTTTATTTGGTTTGGGGTTGA	2491
QY	1179	CCCTCCCACTCGGTGTGAGACTCCAGGACCAAGGACACTTGACACCCCGCTTTTGGCAG	1238
DB	2492	CCCAACCAACATCATATGACTACGATGAGCATTAAGCAATTAAGCCAGAACAGGACAGCAG	2551

QY	1239	GGGCGTGCTCAAGTCGACATCTCGGACCTGTCCCTCATCTGCTGCTGGGCTACAGCAT	1298
DB	2552	GGGAGTTCTCAAAATGTGACATCAAGACCTTCAGATCATTTGTTCTTTGGGATATAGCAT	2611
QY	1299	GCTGCTGATGGTCAAGTGTACTGTGTACGCCATCAAGACCCGAGGGCGTGCCCGAGACCTT	1358
DB	2612	TCTTCTCATGGTCACATGTACTGTGTATGCCATCAAGACTCGGGGTGTACCAGAGAAATTT	2671
QY	1359	CAACGAGGCCAAGGCCCATTCGGCTTCCACATGTATACAACA CACTGCAATTTCTGGCTGGGCTT	1418
DB	2672	TAATGAAGCAAGGCCCATTTGGATTCATATGTATACAGACTTGTATCGTATGGCTTGCCTT	2731
QY	1419	CATCCCATCTTTTTTGGCACCTTCACAGTCAGCGGACAAAGCTCTGTACATCCAGACAACCCAC	1478
DB	2732	CATCCCAATATTTTTTGGCAAGGCCAATCAGCAGAAAGCTCTCATCAAAACACCACCAC	2791
QY	1479	ACTGACGGTCTCGGTGAGTCTGAGCGCTTCAGTGTCCCTGGGGATGCTCTACATGCCCAA	1538
DB	2792	GCTTACAATCTCCATGAACCTAAGTGTCATCAGTGGCGCTGGGGATGCTATACATGCGAA	2851
QY	1539	AGTCTACATCATCTCTTCTCCACCGGAGCAGACGTGCCCAAGCGCAAGCGCAGTCTCAA	1598
DB	2852	AGTGTAATCATCATATTTTCCACCCTGAATCAATGTCCAGAAAACGGAAGCGAAGTTCAA	2911
QY	1599	AGCCGTGGTCAACCGCCGCCACCATGTCTCAACAAGTTTCACACAGAAGGGCAACTTTCAGGCC	1658
DB	2912	GGCCGTGAGTCACAGCAGCCACCATGTCTATCGAGGCTGTACACAAACCCAGTCACAGGCC	2971
QY	1659	CAATGGGGAAGCCAAATTCAGAGCTGTGTGAGAACTCTGGA	1697
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RESULT 9	
AY401209	2611 bp DNA linear GSS'15-DEC-2003
LOCUS	Pan troglodytes GRM7 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION	genomic survey sequence.
ACCESSION	AY401209
VERSION	AY401209.1 GI:39757198
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
AUTHORS	1 (bases 1 to 2611) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 2611)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1..2611 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" <1..>2611 /gene="GRM7" /locus_tag="HCM0814"
gene	
ORIGIN	

Query Match	44.9%	Score 788.2	DB 9	Length 2611
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QY	102	TGCCGAGTCTGGGAGGACAACTTCCATTCGAAGTTGAGCGGCCACGCGTCAAGAAAGG	161	
DB	955	TGCCGAATACTGGGAGGAAAACCTCAACTGCAAGTTGACGATTAGTGGTCAAAAAAGA	1014	
QY	162	AAGCCACATCAAGAGTGACCAACAGAGAGCGCATCGGCAGACATCGGCCCTATGACCA	221	
DB	1015	AGACACAGATCGCAATGCAACAGCAGGAGAGAAATGGAAAAATTCCAACTATGACCA	1074	
QY	222	GGAGGGGAAGGTGCAGTTCGTGATGATGACGCTGTGTACGCCATGGGCCACGCGCTGCACGC	281	
DB	1075	GGAGGGTAAAGTCCAGTTCGTGATTGACGAGTCTATGCTATGGCTCAGCGCCTTCACCA	1134	
QY	282	CATGCACCGTGAACCTGTGTCCGGCCCGGTAGGACTCTGCGCTCGCATGACACCCGTTGA	341	
DB	1135	CATGAAACAAGGATCTCTGTGCTGACTACCGGGGTGTCTGCCAGAGATGAGCAAGCTGG	1194	
QY	342	TGSCACCCAGCTGCTTAAGTACATCAGGAAGCTCAACTTCTCAGGCATTTGGGGGAACCC	401	
DB	1195	AGGCAGAGAGTTGCTGAAGTATATCCGCATGTTAAATTCATGGTAGTCTGGCACTCC	1254	
QY	402	TGTAACCTTCAATGAGAAACGGAGACGCAACCGGGCGCTACGACATCTACAGTACCA---	458	
DB	1255	AGTGATGTTTAAACAAGAACGGGGATGCACCTGGCGGTATGACATCTTTCAGTACCAGAC	1314	
QY	459	ACTGCGCAATGGCTCGGCCGAGTACAAGGTATCATCGGCTCGTGGACAGACACCTGCACCT	518	
DB	1315	CACAAACACAGCAACCCGGGTTACCGTCTGCTCGGCGAGTGGACAGCAACTTTCAGCT	1374	
QY	519	CAGAATAGCGGATGTCAGTGGCCAGGGAGTGGCCAGCAGCTGCGCGGCTCCATCTCGAG	578	
DB	1375	CANNNNNNNNNNNNNGGTAAAGGATCCGNNNNNTACCCCTCAGTGTGCAC	1434	
QY	579	TCGTCCCTCGCAGCCGCGGAGAGAAAGACTGTGAAGGGCATGGCTGCTGCTGGCA	638	
DB	1435	ACTACCATGTGAACGAGCAGAGAAAGACACAGAAAAGGAACCTCTTCTGTGTTGGAC	1494	
QY	639	CTCGAGCCCTGCACCGGGTACAGTACCAGTGCAGCGCTACACCTGTAAAGACTCGCC	698	
DB	1495	CTGTAGCCTTGCATGGTTACCGTACCAGTTACAGTTGATGAGATGACATGCCAGCATTCGCC	1554	
QY	699	CTACGACATCGGCCCAACAGAGAACCGCAAGAGCTGCCAGGCCATCCCATTCGTCAAGTT	758	
DB	1555	CTATGACAGAGGCCCAATGAAAATCGAAACGGAGTGCAGGATATCCCATCATCAAACT	1614	
QY	759	GGAGTGGACTCGCGTGGCGCGTCTGCCCTCTTCTCGCGTGGTGGGCACTCGCGC	818	
DB	1615	GGAGTGGCACTCCCCCTGGGCTGTGATTCCTGTCTCTCGGCAATGTGGGGATCATTCG	1674	
QY	819	CAGCGCTTTCGTGTGTCTAGTTTGTGCGCTACAACGATACCCCATCGTCAAGGGCTC	878	
DB	1675	CACCATCTTTGTCATGSCCATTTTCATCCGCTACAATGACAGGCCCATTTGTTCGGGCTC	1734	
QY	879	GGGCGGGAACTGAGCTACGTGTGCTGGCGGGGATCTTTCTGTGCTACGGCACTACCTT	938	
DB	1735	TGGCGGGAACTNNNNNTATGTTCTTTTTCAGCGGGCATCTTCTTTTGTGTACATCATCTT	1794	
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DB	1795	CCTGATGATGGCCAAACCAATGTGGCAGTGTGTCTTTTCGGGGTGTCTTCTGGGCTT	1854	
QY	999	CGGCATGAGCATCAGTACGGGGCCCTGTGACCAAGACCAACCGCAATTTACCGCATCTT	1058	
DB	1855	GGGTATGTGATCAGTTATGCGGCCCTCTTGACGAAACCAATCGAATTTATCGCATATT	1914	

REFERENCE 1 (bases 1 to 782)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
 1. 782
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 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30360694"
 /tissue_type="whole brain"
 /dev_stages="1, 5 and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_GMO"
 /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 to the protocol of Benton and Davis (1978). The library tag
 is CGAAGTGAAT. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN
 Query Match 40.3%; Score 708; DB 6; Length 782;
 Best Local Similarity 94.0%; Pred. No. 1.5e-153;
 Matches 735; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

772 CCGTGGCGCGTGTGCTCTTCTCTGGCGGTGGTGGCATCGCGGCACGCTGTTCGTG 831
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832 GTGGTCAGCTTTGTGGCTACAAAGATACCCCATCGTCAAGGCTCGGGCGGGAAGCTG 891
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61 GTGGTCAGCTTTGTGGCTACAAAGATACCCCATCGTCAAGGCTCGGGCGGGAAGCTG 120
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892 AGCTACGCTGCTGGCGGATCTTTCTGTGCTACGCACTACCTTCCTCATATCGCA 951
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121 AGCTACGCTGCTGGCGGATCTTTCTGTGCTATGCAACCATCTTCTCATATCGCA 180
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952 GAGCGGACCTGGGACCTGTTCGCTCGCGCGCATCTTCCTAGGCTCGGCATGAGCATC 1011
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181 GAGCTGACCTGGGACCTGTTCCTCTCGCGCATCTTCCTGGGCTGGGCATGAGCATC 240
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 VERSION CN409312.1 GI:47396436
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 711)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, L.W.
 Transcriptional characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
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ORIGIN
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 Best Local Similarity 91.1%; Pred. No. 1.4e-123;
 Matches 637; Conservative 0; Mismatches 60; Indels 2; Gaps 2;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

1 (bases 1 to 1484)

Genoscope.

Direct Submission

Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -

: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

(E-mail : secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

More information available at

<http://www.genoscope.cns.fr/tetraodon>.

Location/Qualifiers

1..1484

/organism="Tetraodon nigroviridis"

/mol_type="mRNA"

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Matches 674; Conservative 0; Mismatches 265; Indels 2; Gaps 1;

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DB 152 ACCTGGTGGCCAGGAGTGGCCAGCAGCTCGCGGCTCCATCTGCAGTCTGCCCTGCCA 211

QY 651 CACCGGTACAGTACCAAGTGGACCGCTACACCTGTGAAGACCTGCCCTAGGACATGG 710

DB 212 CGATGGCTATCAATACCAAGGCTGACCTACACATGCAAGATGTGTGCTTTGATTTGG 271

QY 711 GCCACAGAGAACCGCAGCAGCTGCCAGCCATCCCATCTGCAAGTGGAGTGGGACTC 770

DB 272 ACCCATGAGAAATACACAGCGCTGTGTCCAAATCCCTATAGTCAAAATAGAGTGGAGCTC 331

QY 771 GCCGTGGCCGCTGTGCCCTCTTCTGCGCGTGGTGGGCAATCGCCGACAGCTGTTCGT 830

DB 332 TCCATGGCCAGTCTATCCCTGTGCTAAATTCAGTATCATCGGTATCATGGCCATGTGTTGCT 391

QY 831 GGTGTACAGTTGTGGCTACAGAGTACCCCATGTCAAGGCTCGGCCCGGGAAT 890

DB 392 GGTGTACAGTTGTGGCTACAGAGTACCCCATGTCAAGGCTCGGCCCGGGAAT 451

QY 891 GAGCTACGTGTGTGGCGGCGCATCTTCTGTGTACGCCACTACCTTCTCATGATCGC 950

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BP359939

LOCUS

DEFINITION BP359939 Sugano cDNA library, thalamus Homo sapiens EST 17-SEP-2004

THR00488, mRNA sequence.

ACCESSION BP359939

VERSION BP359939.1 GI:52289953

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 582)

AUTHORS Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

Location/Qualifiers

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DB 61 AAGGATACCCCATCTGTCAAGGCTCGGGCGGGAAGTACGCTGCTGCTGGCGGC 120

QY 913 ATCTTTCTGTGTACGCACTACCTTCTCATATCGAGCGCGGACCTGGGACCTGT 972

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Db 481 CTCATCTGCTGCTGGCTTACAGCATGTGCTCATGCTCACGTGCACCGTGTATGCCATC 540
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Job time : 5991 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 04:25:23 ; Search time 314 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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12	871	49.6	2670	3	US-09-126-280-1
13	860.2	49.0	2635	3	US-09-126-280-3
14	839	47.8	3321	3	US-08-855-146-1
15	839	47.8	3321	3	US-08-855-146-3
16	823.8	46.9	2724	3	US-08-823-110-5
17	823.8	46.9	2724	3	US-08-604-298-5
18	823.8	46.9	3833	3	US-08-823-110-2
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; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481
; FILING DATE: 30-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/626,806
; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-6PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
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; LENGTH: 4095 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:

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; CLONE: SN30
; FEATURE:
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; LOCATION: 463..3198
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Best Local Similarity 99.9%; Pred. No. 0;
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RESULT 2

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US-09-820-809-1
; Sequence 1, Application US/09820809
; Patent No. 6508176
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARI, NIRUPA
; APPLICANT: ROPER, STEPHEN D.
; TITLE OF INVENTION: TASTE RECEPTOR FOR UMAMI (MONOSODIUM GLUTAMATE) TASTE
; FILE REFERENCE: 70373/275576
; CURRENT APPLICATION NUMBER: US/09/820, 809
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,454
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Rattus sp.
```

US-09-820-809-1

Query Match 97.3%; Score 1707.6; DB 4; Length 2838;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	42	AGGGTTGACCGGATCTCTCCAGCGCAGCGTGGACAAACAGCGGCGAAATCTGGTT	101
Db	230	AGGGTTGACCGGATCTCTCCAGCGCAGCGTGGACAAACAGCGGCGAAATCTGGTT	289
Qy	102	TGCCGAGTTCTGGAGGACAACTTCCATTGCAAGTTGAGCGCGCAGCGCTCAAGAAGGG	161
Db	290	TGCCGAGTTCTGGAGGACAACTTCCATTGCAAGTTGAGCGCGCAGCGCTCAAGAAGGG	349
Qy	162	AAGCCACATCAAGAAAGTGACAAACGAGAGCGCATCGGGCAGGACTCGGCCCTATGAGCA	221
Db	350	AAGCCACATCAAGAAAGTGACAAACGAGAGCGCATCGGGCAGGACTCGGCCCTATGAGCA	409
Qy	222	GGAGGGGAAGTTCAGTTCTGATTTGACGCTGTGTACGCCATGGGGCAGCGCTGCACGC	281
Db	410	GGAGGGGAAGTTCAGTTCTGATTTGACGCTGTGTACGCCATGGGGCAGCGCTGCACGC	469
Qy	282	CATGACCGTGACCTGTGTCCGGCGCGTAGGACTCTGCCCTCGCATGGACCCCGTGGA	341
Db	470	CATGACCGTGACCTGTGTCCGGCGCGTAGGACTCTGCCCTCGCATGGACCCCGTGGA	529
Qy	342	TGGCACCCAGCTGCTTAAGTACATCAGGAAAGCTCAACTTCTCAGGCAATTGCGGGGAAACC	401
Db	530	TGGCACCCAGCTGCTTAAGTACATCAGGAAAGCTCAACTTCTCAGGCAATTGCGGGGAAACC	589
Qy	402	TGTAACCTTCAATGAGAACGAGAGCGCACCGGGCGCTACGACATCTACAGTACCAACT	461
Db	590	TGTAACCTTCAATGAGAACGAGAGCGCACCGGGCGCTACGACATCTACAGTACCAACT	649
Qy	462	GGCAATGGCTGGCGGAGTCAAGTCAATCGGCTCGTGAGAGAGACCACTCGACTCAG	521
Db	650	GGCAATGGCTGGCGGAGTCAAGTCAATCGGCTCGTGAGAGAGACCACTCGACTCAG	709
Qy	522	AATAGAGCGGATGCAAGTGGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT	581
Db	710	AATAGAGCGGATGCAAGTGGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT	769
Qy	582	GCCCTGCCAGCCCGGGAGCGAAAGAGACTGTGAAAGGAGTGGCTGTGCTGGGACTG	641
Db	770	GCCCTGCCAGCCCGGGAGCGAAAGAGACTGTGAAAGGAGTGGCTGTGCTGGGACTG	829
Qy	642	CGAGCCCTGACCGGGTACAGTACCAAGTGGACCGCTACAGCTGTAGACCTGCCCCCTA	701
Db	830	CGAGCCCTGACCGGGTACAGTACCAAGTGGACCGCTACAGCTGTAGACCTGCCCCCTA	889
Qy	702	CGACATGCGGCGCCACAGAGAACCGCACGAGCTGCCAGCCCATCCCATCGTCAAGTTGA	761
Db	890	CGACATGCGGCGCCACAGAGAACCGCACGAGCTGCCAGCCCATCCCATCGTCAAGTTGA	949
Qy	762	GTGGAGCTCGCGTGGCGGCTGCTGCTTCTTCTGCGCGTGGTGGGATCGCGGCCAC	821
Db	950	GTGGAGCTCGCGTGGCGGCTGCTGCTTCTTCTGCGCGTGGTGGGATCGCGGCCAC	1009
Qy	822	GCTGTTGCTGGTGGTCACTTGTGCGCTACACGATACCCCGCATCGTCAAGGCTCGG	881
Db	1010	GCTGTTGCTGGTGGTCACTTGTGCGCTACACGATACCCCGCATCGTCAAGGCTCGG	1069
Qy	882	CGGGAACTGAGTACGCTGCTGCTGGCGGATCTTCTGCTGCTAGCGCACTACCTTCT	941
Db	1070	CGGGAACTGAGTACGCTGCTGCTGGCGGATCTTCTGCTGCTAGCGCACTACCTTCT	1129
Qy	942	CATGATCGCAGACCGGACCTGGGACCTGTTGCTCGCGCGCATCTTCTTAGGCTCGG	1001
Db	1130	CATGATCGCAGACCGGACCTGGGACCTGTTGCTCGCGCGCATCTTCTTAGGCTCGG	1189
Qy	1002	CATGAGCATCAGTACCGCGGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTGA	1061
Db	1190	CATGAGCATCAGTACCGCGGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTGA	1249

RESULT 3

PCT-US91-09422-20

; Sequence 20, Application PC/TUS9109422

; GENERAL INFORMATION:

; APPLICANT: Mulvihill, Eileen R.

; APPLICANT: Hagen, Frederick S.

; APPLICANT: Houamed, Khaled M.

; APPLICANT: Almers, Wolfhard

; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend

; STREET: One Market Plaza, Steuart Street Tower

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105-1492

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

Qy	1062	GCAGGGGAAACGGTTCGGTCACTGCCCCCGGCTTTTATCATGACCCCGGCTCTGCAGCTGGCCAT	1121
Db	1250	GCAGGGGAAACGGTTCGGTCACTGCCCCCGGCTTTTATCATGACCCCGGCTCTGCAGCTGGCCAT	1309
Qy	1122	CACCTTCACTCTCATCTCCCTGCGAGCTCTCGGCATCTCGGTGCTGTTGCTGGTGGACCC	1181
Db	1310	CACCTTCACTCTCATCTCCCTGCGAGCTCTCGGCATCTCGGTGCTGTTGCTGGTGGACCC	1369
Qy	1182	CTCCCACTCGGTGGTGGACTTCCAGGACCAACGAGCACTTGAACCCCGCTTTGCCAGGGG	1241
Db	1370	CTCCCACTCGGTGGTGGACTTCCAGGACCAACGAGCACTTGAACCCCGCTTTGCCAGGGG	1429
Qy	1242	CGTGTCAAGTGGAGCATCTCGGACCTGTCCCTCATCTGCTGCTGCTGGGTACAGCATGCT	1301
Db	1430	CGTGTCAAGTGGAGCATCTCGGACCTGTCCCTCATCTGCTGCTGCTGGGTACAGCATGCT	1489
Qy	1302	GCTGATGTGACGTGTACTGTGTCGCGCATCAAGACCCGAGGCGTGGCCGAGACCTTCAA	1361
Db	1490	GCTGATGTGACGTGTACTGTGTCGCGCATCAAGACCCGAGGCGTGGCCGAGACCTTCAA	1549
Qy	1362	CGAGGCCAAGCCCATCGGCTTCCACCATGTACACCACTGCAATTTGCTGGCTGGCTTCA	1421
Db	1550	CGAGGCCAAGCCCATCGGCTTCCACCATGTACACCACTGCAATTTGCTGGCTGGCTTCA	1609
Qy	1422	CCCCATCTTTTGGACCTCAGTCAAGTCAAGTGTATCATCCAGAACCACTCACT	1481
Db	1610	CCCCATCTTTTGGACCTCAGTCAAGTGTATCATCCACCTGCAATTTGCTGGCTGGCTTCA	1669
Qy	1482	GACGCTCTCCGTGAGTCTGAGGCTTCAAGTGTCCCTGGGATGCTCTACATGCCCAAGT	1541
Db	1670	GACGCTCTCCGTGAGTCTGAGGCTTCAAGTGTCCCTGGGATGCTCTACATGCCCAAGT	1729
Qy	1542	CTACATCATCTCTTCCACCCGAGCAGAAAGTGTCCCAAGGCGCAGCTCTCAAGC	1601
Db	1730	CTACATCATCTCTTCCACCCGAGCAGAAAGTGTCCCAAGGCGCAGCTCTCAAGC	1789
Qy	1602	CGTGTCAACCCCGCCACCATGTCCAAAGTGTCAACAGAGGGCAACTTCAGGCCCAA	1661
Db	1790	CGTGTCAACCCCGCCACCATGTCCAAAGTGTCAACAGAGGGCAACTTCAGGCCCAA	1849
Qy	1662	TGGGGAGCAAAATCAGAGCTGTGTGAACTTGAGAGCCCGAGCGCTGGCTACCAACA	1721
Db	1850	TGGGGAGCAAAATCAGAGCTGTGTGAACTTGAGAGCCCGAGCGCTGGCTACCAACA	1909
Qy	1722	GACCTACCTGCTACCTACACCAACCATGCTCTAG	1755
Db	1910	GACCTACCTGCTACCTACACCAACCATGCTCTAG	1943

APPLICATION NUMBER: PCT/US91/09422
FILING DATE: 19911212
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,007
FILING DATE: 18-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648,481
FILING DATE: 30-JAN-1991
APPLICATION DATA:
APPLICATION NUMBER: US 07/626,806
FILING DATE: 12-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-6PC
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: SR13
PCT-US91-09422-20

Query Match 86.4%; Score 1516.4; DB 5; Length 2426;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 42 AGGTTTCGACCGATATCTCTCAGCCGACGCTGGACAAACAGCGCCGCAACATCTGGTT 101
Db 738 AGGTTTCGACCGATATCTCTCAGCCGACGCTGGACAAACAGCGCCGCAACATCTGGTT 797

Qy 102 TGCCGAGTCTGGGAGGCACTTCCATTGCAAGTTGAGCGCCGACGCGCTCAAGAGGG 161
Db 798 TGCCGAGTCTGGGAGGCACTTCCATTGCAAGTTGAGCGCCGACGCGCTCAAGAGGG 857

Qy 162 AAGCCACATCAAGAGTGACCAACCCGAGAGCGCATCGGGGAGGACTCGGCTATGAGCA 221
Db 858 AAGCCACATCAAGAGTGACCAACCCGAGAGCGCATCGGGGAGGACTCGGCTATGAGCA 917

Qy 222 GGAGGGGAAGTGCGATTTGTTGATGACGCTGTGTAAGCGCATGGGCCACGCGCTGACGC 281
Db 918 GGAGGGGAAGTGCGATTTGTTGATGACGCTGTGTAAGCGCATGGGCCACGCGCTGACGC 977

Qy 282 CATGACCGTGACCTGTCTCCGGCCGGTAGGACTCTGGCTCGCATGGACCCCGTGA 341
Db 978 CATGACCGTGACCTGTCTCCGGCCGGTAGGACTCTGGCTCGCATGGACCCCGTGA 1037

Qy 342 TGCCACCCAGCTGCTTAAGTATACAGGAACGTCAACTTCTCAGGCATTTGGGGGAACCC 401
Db 1038 TGCCACCCAGCTGCTTAAGTATACAGGAACGTCAACTTCTCAGGCATTTGGGGGAACCC 1097

Qy 402 TGTAACCTTCAATGAGAACGAGACGCAACCGGGCGCTACGACATCTACAGTACCAACT 461
Db 1098 TGTAACCTTCAATGAGAACGAGACGCAACCGGGCGCTACGACATCTACAGTACCAACT 1157

Qy 462 GGGCAATGGCTCGGCCGAGTACAAAGGTCTGGCTCGTGGACAGACACCTGCACTCAG 521
Db 1158 GGGCAATGGCTCGGCCGAGTACAAAGGTCTGGCTCGTGGACAGACACCTGCACTCAG 1217

Qy 522 AATAGAGCGGATGCGAGTGCCAGGAGTGCGCAGCAGCTGCGCGCTCCATCTCGAGTCT 581
Db 1218 AATAGAGCGGATGCGAGTGCCAGGAGTGCGCAGCAGCTGCGCGCTCCATCTCGAGTCT 1277

Qy 582 GCCCTGCCAGCCCGGGGAGCGGAAGAAGATGTGTGAAGGGCATGTGCTGCTGCGCACTG 641
Db 1278 GCCCTGCCAGCCCGGGGAGCGGAAGAAGATGTGTGAAGGGCATGTGCTGCTGCGCACTG 1337

RESULT 4

US-09-641-318-1

; Sequence 1, Application US/09641318

; Patent No. 6384205

; GENERAL INFORMATION:

; APPLICANT: BELAGAJE, RAMA M.

; WU, SU

Qy 642 CGAGCCCTGCACCGGGTACCAAGTGGAGCCGCTACACCTGTGAAGACCTGCCCCCTA 701
Db 1338 CGAGCCCTGCACCGGGTACCAAGTGGAGCCGCTACACCTGTGAAGACCTGCCCCCTA 1397

Qy 702 CGACATCGGCCCCACAGAGAACCGACAGAGTGCGACGCCATCCCATCGTCAAGTTGGA 761
Db 1398 CGACATCGGCCCCACAGAGAACCGACAGAGTGCGACGCCATCCCATCGTCAAGTTGGA 1457

Qy 762 GTGGGACTCGCGTGGGCGGCTGCTGCCCTCTTCTGGCGTGGTGGGCATCGCGCGCAC 821
Db 1458 GTGGGACTCGCGTGGGCGGCTGCTGCCCTCTTCTGGCGTGGTGGGCATCGCGCGCAC 1517

Qy 822 GCTGTTGCTGCTGCTCACGTTTGTGCGCTACAAAGATACCCCATCGTCAAGGCTCGGG 881
Db 1518 GCTGTTGCTGCTGCTCACGTTTGTGCGCTACAAAGATACCCCATCGTCAAGGCTCGGG 1577

Qy 882 CCGGAACTGAGCTACGCTGCTGCTGGCGGGCATCTTCTGTGTACGCCACTACCTTCCT 941
Db 1578 CCGGAGCTGAGCTACGCTGCTGCTGGCGGGCATCTTCTGTGTACGCCACTACCTTCCT 1637

Qy 942 CATGATCGAGAGCGGACCGCTGGGAGCTGTTGCTCGCGCATCTTCTAGGCTCGG 1001
Db 1638 CATGATCGAGAGCGGACCGCTGGGAGCTGTTGCTCGCGCATCTTCTAGGCTCGG 1697

Qy 1002 CATGAGCATGAGCTACGCGGCCCTGTGTAACCAAGACCAACCGCATTTACCGCATCTTGA 1061
Db 1698 CATGAGCATGAGCTACGCGGCCCTGTGTAACCAAGACCAACCGCATTTACCGCATCTTGA 1757

Qy 1062 GCAGGGCAACGCTGCTGAGTGCCTCGCGCTTTCATCAGCCCGGCTCGAGCTGGCCAT 1121
Db 1758 GCAGGGCAACGCTGCTGAGTGCCTCGCGCTTTCATCAGCCCGGCTCGAGCTGGCCAT 1817

Qy 1122 CACCTTCATCTCATCTCCCTGACGCTGCTGGCATCTGCGTGTGTTCTGCTGGGACCC 1181
Db 1818 CACCTTCATCTCATCTCCCTGACGCTGCTGGCATCTGCGTGTGTTCTGCTGGGACCC 1877

Qy 1182 CTCCCACTCGGTGTGAGACTTCCAGGACCAACGAGACACTTGAACCCCGCTTTGCGAGGG 1241
Db 1878 CTCCCACTCGGTGTGAGACTTCCAGGACCAACGAGACACTTGAACCCCGCTTTGCGAGGG 1937

Qy 1242 CGTCTCAAGTGCGACATCTCGGACCTGCTCCCTCATCTGCTGCTGGGCTACAGCATGCT 1301
Db 1938 CGTCTCAAGTGCGACATCTCGGACCTGCTCCCTCATCTGCTGCTGGGCTACAGCATGCT 1997

Qy 1302 GCTGATCGTCAAGTGACTGTGACGCGCATCAAGCCGAGCGCTGCCGAGACCTTCAA 1361
Db 1998 GCTGATCGTCAAGTGACTGTGACGCGCATCAAGCCGAGCGCTGCCGAGACCTTCAA 2057

Qy 1362 CGAGGCCAAGCCCATCGGCTTTCACCATGTACCCACCTGCAATTGCTTGGCTGGGCTTCAT 1421
Db 2058 CGAGGCCAAGCCCATCGGCTTTCACCATGTACCCACCTGCAATTGCTTGGCTGGGCTTCAT 2117

Qy 1422 CCCCATCTTTTGGCACTCAAGTACGCGGCAAGCTGTATCATCAAGCAACCACT 1481
Db 2118 CCCCATCTTTTGGCACTCAAGTACGCGGCAAGCTGTATCATCAAGCAACCACT 2177

Qy 1482 GACGGTCTCCGTGAGTCTGAGCGCTTCAAGTGTCCCTGGGATGCTTACATGCCCAAGT 1541
Db 2178 GACGGTCTCCGTGAGTCTGAGCGCTTCAAGTGTCCCTGGGATGCTTACATGCCCAAGT 2237

Qy 1542 CTACATCATCTCTTCCA 1559
Db 2238 CTACATCATCTCTTCCA 2255

RESULT 4

US-09-641-318-1

; Sequence 1, Application US/09641318

; Patent No. 6384205

; GENERAL INFORMATION:

; APPLICANT: BELAGAJE, RAMA M.

; WU, SU

TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
AND RELATED NUCLEIC ACID COMPOUNDS

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: ELI LILLY AND COMPANY

STREET: LILLY CORPORATE CENTER

CITY: INDIANAPOLIS

STATE: INDIANA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/641,318

FILING DATE: 18-Aug-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/816,178A

FILING DATE: 12-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: GAYLO, PAUL J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-10579

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 276-0756

TELEX: (317) 276-3861

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3431 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 26..2761

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-641-318-1

Query Match 83.8%; Score 1470.8; DB 3; Length 3431;

Best Local Similarity 91.1%; Pred. No. 0;

Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY	42	AGGGTTTCAGACCATCTCTCCAGCGGACGCTGACACCAACAGCGCAACATCTGGTT	101
DB	1051	AGGCTTCGACCCCTACTCTCCAGCGGACGCTGACACCAACAGCGGCAACATCTGGTT	1110
QY	102	TGCCAGATTCTGGAGGACAACTTCCATTGCAAGTTGAGCCGCCACGCGCTCAAGAAGGG	161
DB	1111	TGCCAGATTCTGGAGGACAACTTCCACTGCAAGCTGAGCCGCCACGCGCTCAAGAAGGG	1170
QY	162	AAGCACATCAAGATGTGACCAACCGAGAGGCGATCGGGGAGGACTGGGCCCTATGAGCA	221
DB	1171	CAGCCACGTCAAGAAGTGACCAACCGGTGAGCGAATTGGGCAAGGATTTCAGCTTATGAGCA	1230
QY	222	GGAGGGAGGTGAGTTCGTGATGAGCTGTGTACGCCCATGGGCGCAGCGCTGCACGC	281
DB	1231	GGAGGGAGGTGAGTTCGTGATGAGCTGTGTACGCCCATGGGCGCAGCGCTGCACGC	1290
QY	282	CATGCACCGTGACCTGTGTCCGGCGCGGTAGGACTCTGCCCTCGCATGGACCCCGGTGGA	341
DB	1291	CATGCACCGTGACCTGTGTCCGGCGCGGTAGGACTCTGCCCTCGCATGGACCCCGGTGGA	1350
QY	342	TGGCACCCAGCTGCTTAAGTACATCAGGAACTCAACTCTCAGGATTCGGGGGAAACC	401
DB	1351	TGGCACCCAGCTGCTTAAGTACATCAGGAACTCAACTCTCAGGATTCGGGGGAAACC	1410
QY	402	TGTACCTTCATGAGACGGAGCGCACCGGGCGCTACGACATCATCAGTACCAACT	461
DB	1411	TGTACCTTCATGAGATGGAGATGCGCCCTGGGCGCTATGACATCTACCAATACCACT	1470

Db 2551 CTACATCATCTCTTCCACCCGGAGCAGAAAGTGGCCCAAGCGCAAGCGCAGCTCAAAGC 2610
Qy 1602 CGTGTACCCGCGCCACATGTCCAAAGTTTACACAGAGGCGCACTTCAGGCCCAA 1661
Db 2611 CGTCGTTACGGCGGCGCACCATGTCCAAAGTTTACAGCAGAGGCGCACTTCAGGCCCAA 2670
Qy 1662 TGGGGAAGCCAAATCAGAGCTGTGTGAGAACTGTGAGACCCAGCGCTGGGTACCAAAACA 1721
Db 2671 CGGAGAGCCCAAGTCTGAGCTCTGGAGAACCTTGAGGCCCGCAGCGCTGGCCACCAAAACA 2730
Qy 1722 GACCTACGTCACTTACACCAACCACTGCTCATCTAG 1755
Db 2731 GACTTACGTCACTTACACCAACCACTGCACTAG 2764
RESULT 5
US-09-641-318-3
; Sequence 3, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; WU, SU
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELI LILLY AND COMPANY
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: INDIANA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,318
; FILING DATE: 18-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,178A
; FILING DATE: 12-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: GAYLO, PAUL J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10579
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-641-318-3
Query Match 83.8%; Score 1470.8; DB 3; Length 3431;
Best Local Similarity 74.2%; Pred. No. 0;
Matches 1271; Conservative 291; Mismatches 152; Indels 0; Gaps 0;
Qy 42 AGGGTTTCAGCCGATATCTTCAGCGCGCAGCGTGGACAAACAGCGCGCAACATCTGGTT 101
Db 1051 AGGCUUACCCGCUAUUUCUCCAGCGCGCAGCGUGGACAAACAGCGCGCAACUUGGU 1110
Qy 102 TGCCAGTTCTGGGAGGACAACTTCATTGCAAGTTGAGCGGCCACCGGCTCAAGAAGGG 161
Db 1111 UGCCGAGUUCUGGGAGGACAAUUCACUGCAAGCUGAGCGGCCCAAGAGGG 1170

Qy 162 AAGCCACATCAAGAAGTGCACCAACCGAGAGCGCATCGGCGCAGGACTCGGCTTATGAGCA 221
Db 1171 CAGCCACGUCUAAGAAGUGCACCACCGUGAGCGAAUUGGCGAGUACUAGCUUAGAGCA 1230
Qy 222 GGAGGGGAAGGTGAGTTCGTGATTGACGTGTGTACGCCATGSGGCCACCGGCTGCAGCG 281
Db 1231 GGAGGGGAAGGUGCAGUUGUUGAUCGAGUUGCGUGUACCGCAUGGGGCCACGCGCUGCAGCG 1290
Qy 282 CATGSCACCGTACCTGTCCCGSCCGGTAGGACTCTGCGCTCGCATGGACCCCGCTGGA 341
Db 1291 CAUGCACCUGAGCCUGUGUCCCGCGCGUGGGGUCUCUGCCCGCGCAUGAGACCCUGUAGA 1350
Qy 342 TGGCACCACAGCTGCTTAAGTACATCAGGAAACGTCAACTTCTCAGGCAATGCGGGGAACCC 401
Db 1351 UGGCACCACAGCUGCUUAAAGUACAUCCGAAAGCUGCAACUUCUCAGGCAUCGCGAGGGAACCC 1410
Qy 402 TGTAACCTTCAATGAGAACCGGAGACGACCCGGGGCGCTACGACATCTACAGTACCAACT 461
Db 1411 UGUGACCUCUCAAUGAGAAUGGAGAUUGCGCCUGGGCGCUUAGCAUCAUCCAAUACCAAGCU 1470
Qy 462 GCGCAATGGCTCGSCCGAGTACAAAGTTCATCGGCTCGTGACAGACACCACTGCACTCAG 521
Db 1471 GCGCAACAUUCCCGCAGUACAAAGUUAUUGGCUCCUGAGACCAUCCUGCACTUUG 1530
Qy 522 AATAGAGCGGATGAGTGGCCAGGGAGTGCCAGAGCTGCGCGCTCCATCTCGAGTCT 581
Db 1531 AAUAGAGCGGAGUACUGCGCGGGAGCGGAGCAGCAGCUGCGCGCUCCAGCAGCUCU 1590
Qy 582 GCCCTGCGAGCCCGGGAGGAGAAAGACTGTGAAAGGGCATGSGCTTGTGCTGGCACTG 641
Db 1591 GCCCUGCCAAACCGGGUGAGCGGAAGACAGUAGAGGGAUGGCUUGCUGCGGCAUG 1650
Qy 642 CGAGCCCTGCGACCGGTTACAGTACCAAGTGGACCGCTACACCTGTGAAGACTCTCCCTA 701
Db 1651 CGAGCCUUGCAGAGGUACAGUACAGGUGGACCGCUACACCUUAGAGCGUUCUCCUA 1710
Qy 702 CGACATCGCGCCACAGAGAACCGCAGAGCTGCAGCCCATCCCATCTGCTCAAGTTGGA 761
Db 1711 UGACAUUGCGGCCACAGAGAACCGCAGCGGCGCGGCCCAUCCCAUCAUAGCUUGA 1770
Qy 762 GTGGGACTCGCGGTGGGCGGTGCTGCCCTCTTCTGCGCGTGTGGGCATCGCGCGCAC 821
Db 1771 GUGGGGCGCGCCCGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1830
Qy 822 GCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
Db 1831 GUUUGUGUGUGUGAUCUUCUUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG 1890
Qy 882 CCGGGAACGTGAGCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941
Db 1891 CCGUGAACUGAGCUACGUG 1950
Qy 942 CATGATCGAGAGCCGCGACCTGGGACCTGTTGCTGCGCGGATCTCTCTAGGGCTCGG 1001
Db 1951 CAUGAUCGUGAGCCCGACCUUGGACCUUGGACCUUGGACCUUGGACCUUGGACCUUGG 2010
Qy 1002 CATGAGCATCAGCTACCGCGCCCTGCTGACCAAGACCAACCGCATTTACCGCATCTTGA 1061
Db 2011 GAUGAGCAUCAUUGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2070
Qy 1062 GCAGGGCAACCGTTCGGTTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1121
Db 2071 GCAGGGCAACCGUG 2130
Qy 1122 CACTTTCATCT 1181
Db 2131 CACCTUAGCCUACUUCGUG 2190
Qy 1182 CTCCCACTCGGTGTGAGCTTCCAGGACCAACGAGCACTTGAACCCCGCTTTCGAGGGG 1241
Db 2191 CUCCACUUG 2250
Qy 1242 CGTCTCAAGTGCAGCATCTCGGACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1301

Db 2036 CCGTGAACAGCTAGCTGCTGCTGGCAGGCATCTTCTGTGCTATGCCACCACTTCTCT 2095
Qy 942 CATGATCCGACAGCGGACCTGGGGAAGTGTCTCGCCGCATCTTCTAGGGCTCGG 1001
Db 2096 CATGATCGCTAGCGCGGACCTTGGACCTGCTGCTGCGCGGAATCTTCTGGGACTAGG 2155
Qy 1002 CATGAGCATCAGCTACGCGGCGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGA 1061
Db 2156 GATGAGCATCAGCTATGAGCGCTGCTGACCAAGACCAACCGCATCTTACCGCATCTTGA 2215
Qy 1062 GCAGGCAAAACGGTCGGTCACTGCGCCCGCTTTTATCAGCCCGCGCTGCGAGCTGGCCAT 1121
Db 2216 GCAGGCAAGCGCTCGGTCACTGCGCCCGCATCTTATCAGCCCGCTTACAGCTGGCCAT 2275
Qy 1122 CACCTTCATCTCATCTCCCTGCGAGCTGCTCGGCACTCTGCGTGTGGTTCGTTGGTGAACC 1181
Db 2276 CACCTTCAGCCCTCATCTCGCTGCGAGCTGCTGGGCACTCTGTGTGGTTCGTTGGTGAACC 2335
Qy 1182 CTCCACCTCGGTGGTGGACTTCCAGGACCAACCGGACACTTGACCCCGCTTTGCGAGGG 1241
Db 2336 CTCCACCTCGGTGGTGGACTTCCAGGACCAACCGGACACTTGACCCCGCTTTGCGAGGG 2395
Qy 1242 CGTGTCAAGTGCACATCTCGGACCTGTCCTCATCTGCTGCTGGGCTACAGCATGCT 1301
Db 2396 TGTGCTCAAGTGTGACATCTCGGACCTGCTGCTCATCTGCTGCTGGGCTACAGCATGCT 2455
Qy 1302 GCTGATGCTACGCTGCTACTGTGAGCCATCAAGACCGGAGCGGTGCGGAGACTTCAA 1361
Db 2456 GCTATGCTACGCTGACCGCTGTATGCCATCAAGACCGGAGCGGTGCGGAGACTTCAA 2515
Qy 1362 CGAGGCCAAGCCCATCGGCTTCAACATGACCACTGCACTTGTCTGGCTGGGCTTTCAT 1421
Db 2516 TGAGGCCAAGCCCATTGGCTTCAACATGACCACTTGCATGCTGCTGGCTGGGCTTTCAT 2575
Qy 1422 CCCCATCTTTTGGCACTCAGCTAGCGACGACGACAGCTGTACATCCAGACAAACACACT 1481
Db 2576 CCCCATCTTTTGGCACTCAGCTAGCGACGACGACGACGCTGTACATCCAGACGACGAGCT 2635
Qy 1482 GACGGTCTCGTGTAGCTGAGGGCTTCACTGTCTCTGGGATGCTCTACATGCCCAAGT 1541
Db 2636 GACGGTCTCGTGTAGCTGAGGGCTTCACTGTCTCTGGGATGCTCTACATGCCCAAGT 2695
Qy 1542 CTACATCATCTCTTCCACCGGAGCAGAAAGTGTCCCAAGCGCAAGCGAGCTCTCAAAGC 1601
Db 2696 CTACATCATCTCTTCCACCGGAGCAGAAAGTGTCCCAAGCGCAAGCGAGCTCTCAAAGC 2755
Qy 1602 CGTGTCAACCGCGCCACCATGTCCAAAGTTTCAACAGAGGCACTTTCAGGCCCCAA 1661
Db 2756 CGTGTCAACCGCGCCACCATGTCCAAAGTTTCAACAGAGGCACTTTCAGGCCCCAA 2815
Qy 1662 TGGGGAAGCCAAATCAGAGCTGTGTGAAACCTTGAGAGCCCGGCTGGGCTAGCCAAACA 1721
Db 2816 CGAGAGGCCAAATCAGAGCTGTGTGAAACCTTGAGAGCCCGGCTGGGCTAGCCAAACA 2875
Qy 1722 GACCTACGCTACCTACACCAACCATGCACTCTAG 1755
Db 2876 GACTTACGCTCACTTACACCAACCATGCACTCTAG 2909

RESULT 7
US-09-820-809-14
; Sequence 14, Application US/09820809
; Patent No. 6508176
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARI, NIRUPA
; APPLICANT: ROBER, STEPHEN D.
; TITLE OF INVENTION: TASTE RECEPTOR FOR UMAMI (MONOSODIUM GLUTAMATE) TASTE
; FILE REFERENCE: 70373/275576
; CURRENT APPLICATION NUMBER: US/09/820,809
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,454
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 3884
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-820-809-14

Query Match 83.8%; Score 1470.8; DB 4; Length 3884;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

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Qy 102 TCCGAGTTCTGGGAGAGCAACTTCCATTGCAAGTTGAGCGCGCACCGCTCAAGAGGG 161
Db 1256 TCCGAGTTCTGGGAGAGCAACTTCCATTGCAAGTTGAGCGCGCACCGCTCAAGAGGG 1315
Qy 162 AAGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGCGAGGACTCGGCTATGAGCA 221
Db 1316 AAGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGCGAGGACTCGGCTATGAGCA 1375
Qy 222 GAGGGGAAGGTTCAGTTCTGTGATTGACGTGTGTACGCCATGAGGCGCAACGCTGCGC 281
Db 1376 GAGGGGAAGGTTCAGTTCTGTGATTGACGTGTGTACGCCATGAGGCGCAACGCTGCGC 1435
Qy 282 CATGCACGTTGACCTGTCCTCGGCGCGGTAGGACTCTGCCCTCGCATGAGACCCGCTGGA 341
Db 1436 CATGCACGTTGACCTGTCCTCGGCGCGGTAGGACTCTGCCCTCGCATGAGACCCGCTGGA 1495
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Db 1796 CGAGCCCTGCAACCGGTTACAGTACCAAGTGGACCGCTACACCTGTAGAGCTGCCCTTA 1855
Qy 702 CGACATCGGCGCCACAGAGAAACCGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGGA 761
Db 1856 TGACATCGGCGCCACAGAGAAACCGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGGA 1915
Qy 762 GTGGGACTCGCGGCGGCGGCTGCTGCGCTCTTCTGCGCGTGTGGGCACTGCGGCGCAC 821
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Qy 882 CCGGGAACCTGAGCTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941
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Qy	882	CCGGAACTGAGCTACGTGCTGTGGGGGCATCTTTCTGTGCTACGCCACTACCTTCCT	941
Db	1866	CCGTGAATGAGCTACGTGCTGTGGCAGGCATCTTCTGTGCTATGCCACCACTTCCT	1925
Qy	942	CATGATCGCAGAGCGGACCTTGGGACCTGTTCGCTCGCGGCATCTTCTAGGCTCGG	1001
Db	1926	CATGATCGCTGAGCCGACCTTGGCACTGTCTGCTGCGCGAATCTTCTGGGACTAGG	1985
Qy	1002	CATGAGCATCAGCTACGCGGCCCTGTCTGACCAAGACCAACCGCATTTACCGCATCTTTGA	1061
Db	1986	GATGAGCATCAGCTATGAGCCCTGCTCAACCAAGACCAACCGCATCTACCGCATCTCGA	2045
Qy	1062	GCAGGGCAAAACGTCGTGTCAGTCCCCCGCGTTTCATCAGGCCGGCCTCGCAGCTGGCCAT	1121
Db	2046	GCAGGGCAAGCGCTCGTCTAGTGCAGTCCCAACGCTTCATCAGGCCCGCCTCACAGCTGGCCAT	2105
Qy	1122	CACCTTCACTCCTCATCTCCCTGACGTGCTCGGCATCTGGTGTGGTTCGTGGTGACCC	1181
Db	2106	CACCTTCAGCCTCATCTGCTGCACTGCTGGGCATCTGTGTGTGTTTGTGGTGACCC	2165
Qy	1182	CTCCACTCTCGTGTGGACTTTCACGAGCAACCAACGACACTTGTACCCCCGCTTTTGCCAGGGG	1241
Db	2166	CTCCCACTCGTGTGGACTTTCACGAGCAACGAGCGACACTCGACCCCCGCTTCGCCAGGGG	2225
Qy	1242	CGTGCCTAAGTGCAGCATCTTCGGAACCTGTGCCCTCATCTGCCCTGTGGGCTACAGCATGCT	1301
Db	2226	TGTGCTCAAGTGTGACATCTCGGACCTGTTCGCTCATCTGCTGTGGGCTACAGCATGCT	2285
Qy	1302	GCTCATGCTCAGTGTACTGTGTACGCCATCAAGACCCGAGGGGTGCCGAGACCTTCAA	1361
Db	2286	GCTCATGCTCAGTGTACGTCACCGTGTATGCATCAAGACAGCGCGCTGCCGAGACCTTCAA	2345
Qy	1362	CGAGGCCAAGCCCATCGGCTTACCATTGTACCAACCTGTATGTCTGGCTGGCTTCAT	1421
Db	2346	TGAGGCCAAGCCCATCGCTTACCATTGTACCACTGTACCATCTGCTGTGGCTGGCTTCAT	2405
Qy	1422	CCCATCTTTTGGCACTTCAGTTCAGCGGACAGCTGTACATTCAGACACCACTCACT	1481
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Qy	1482	GACGGTCTCCGTGAGTCTGACGCTTCAGTGTCTCCTGGGATGCTCTPACATGCCAAAGT	1541
Db	2466	GACGGTCTCCGTGAGTCTGACGCTTCGTTGTCTCCTGGGATGCTCTACATGCCAAAGT	2525
Qy	1542	CTACATCATCTCTTCCACCCGAGCAGAAAGTGTGCCCAAGCGCAAGCGCAGTCTCAAAGC	1601
Db	2526	CTACATCATCTCTTCCACCCGAGCAGAAAGTGTGCCCAAGCGCAAGCGCAGTCTCAAAGC	2585
Qy	1602	CGTGGTCACCGCGCCACCATGTCCACAAAGTTCCACAGAAAGGCAATCTTCAGGCCCAA	1661
Db	2586	CGTGGTTACCGCGGCCACCATGTCCACAAAGTTCCACAGAAAGGCAATCTTCAGGCCCAA	2645
Qy	1662	TGGGGAAAGCCAAATCAGAGCTGTGTGAGAACTCGGAGACCCACGCGCTGGCTACCAACA	1721
Db	2646	CGGAGAGGCCAAGTCTGAGCTCTCGGAGAACCTTGAGGCCCCACGCGCTGGCCCAACA	2705
Qy	1722	GACCTACGTCACTTACACCAACCATGGCAATC	1752
Db	2706	GACTTACGTCACTTACACCAACCATGCAATC	2736

RESULT 9

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RES001 3
US-09-817-464-1
; Sequence 0, Application US/09817464
; Patent No. 6515107
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Rainer
; APPLICANT: Lindaur, Kristen
; APPLICANT: Püttner, Irene
; APPLICANT: Knöpfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,

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Db 1456 GTGATGTTCAACAGAGAACGGGATCGCCCGGGGGTACGACATCTTCCAGTACCGGCG 1515
Qy 463 CGCAATGGCTGGC-----CGAGTACAGGTTCATCGGCTGGTGGACAGACCACTG 513
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Qy 514 CACCTCAGAAATAGCGGATGCAAGTGGCCAGGGAGTGGCCAGCAGCTGCCGGCTCAATC 573
Db 1576 AGACTGGATGGAGGCCCTGAGTGGTGTGGGACCCCCACGAGGTGCCCTGCTCTGTG 1635
Qy 574 TGCAGTCTGCCCTGCAGCCCGGGGAGCGAAGAAAGACTGTGAAGGGCATGGCTTGTGTC 633
Db 1636 TGCAGCTGCCCTGCAGCCCGGGGAGCGAAGAAAGATGTTGAAGGGGTGCCCTGCTGT 1695
Qy 634 TGGCACTGGAGCCCTGCAGCCGGGTACCAAGTACCAAGTGGACCGCTACACCTGTAAAGACC 693
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Qy 694 TGCCTCTAGCAGATCGGCCCCACAGAGAACCGCAGCTGCCAGCCCATCCCATCGTC 753
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Qy 754 AAGTTGGAGTGGGACTCGCCGTGGCCGTGCTTCCCTTCCCTGGCCGTGGTGGGCATC 813
Db 1816 CGCCTGAGTGTCTCCCTTGGGCGCCCGCGCTCTCTTGGCCGTGCTGGGCATC 1875
Qy 814 GCCGCCAGCTGTTCTGGTGGTGTCACTGTTGTGGCTACACGATACACCCCATGTCAAG 873
Db 1876 GTGGCCACTACCAACGGTGTGGCCACCTTTCGTGGGTACAAACACAGCCCATGTTCGG 1935
Qy 874 GCCTCGGGCCGGAACCTGAGCTACGTGCTGGCGGGCAGCTTCTGTGTACGCCACT 933
Db 1936 GCCTCGGGCCGAGACTGAGCTACGTGCTCTCTCACCGGCACTTCTCTCATACGCCATC 1995
Qy 934 ACCTTCTCATGATCGCAGAGCCGACCTGTGGGACCTGTTCGCTCCGCCGATCTTCCTA 993
Db 1996 ACCTTCTCATGCTGCTGAGCCTGGGCGCGGGTCTGTGCCGCGCGAGGCTCTTCCTG 2055
Qy 994 GGGCTCGGATGAGCATGAGTACCGCGGCTGTGTCAGACAAACGAGATTTACGCC 1053
Db 2056 GGGCTGGGACGACCTCAGCTACTCTGCCCTGTCTACCAAGACCAACCGTATCTACGCC 2115
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Db 2116 ATCTTTGAGCAGGCAACGGTGGTCACTGAGTCCCGCTTTCATCAGCCCGGCTCGAG 2175
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Db 2296 GCCAGAGGGTGTCAAGTGGGACATGTCGGATCTGTCTCATCGGCTGGGCTGAGGCTAC 2355
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Db 2656 CTCAAGGCCACCTCCACGGTGGCAGCCGCCACCAA 2690

RESULT 11
US-09-277-858-1
; Sequence 1, Application US/09277858
; Patent No. 6362316
; GENERAL INFORMATION:
; APPLICANT: Dagget, Lorrie
; Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; SUBTYPE mGluR6, NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/277,858
; FILING DATE: 26-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,875
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9921
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2961 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 85..2718
; OTHER INFORMATION: /product= "Human Metabotropic
; Glutamate Receptor Subtype mGluR6"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-277-858-1

Query Match 50.2%; Score 880.6; DB 3; Length 2961;
Best Local Similarity 72.5%; Pred. No. 1.1e-192;
Matches 1156; Conservative 0; Mismatches 430; Indels 9; Gaps 1;
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Qy 103 GCCGAGTCTGGGAGGACAACTTCATTGCAAGTTGAGCCGCCACCGCTCAAGAGGGA 162

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Db 1216 GATTCACCCGCAATGCAACGAGCGAGGAACGATCGGCCGGGACTCTCACTACGAGCAG 1275
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Db 1336 ATGCACCGCGCTCTGCCCTGGGCACACAGGCCGTGTGCCCGGATGGAACCCACCGAT 1395
Qy 343 GGCACCCAGCTGTTAAGTATCATCAGAAAGCTCAACTTCTCAGGCAATTCGGGGAAACCTC 402
Db 1396 GGGCGGATCTTCTGCAGTATCATCCAGAGCTGTCCGCTTCAACGGCAGCGCAGAAACCCCT 1455
Qy 403 GTAACCTTCAATGAGAACGAGACGACCGGGGCGCTACGACATCTACCACTACCACTG 462
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Qy 463 CGCAATGGCTCGGC-----CGAGTACAAAGTCACTCGGCTCGTGGACAGACCACTG 513
Db 1516 ACCAATGGCAGTGCCAGCAGTGGCGGTACAGGCAGTGGGCCAGTGGGCAGAGACCTC 1575
Qy 514 CACCTCAGAAATAGCGGATGAGTGGCCAGGAGTGGCCAGCAGTGGCCGCGTCCATC 573
Db 1576 AGACTGGATGTGAGGCGCTGCAGTGCTGTGGCAGCCCGACAGAGTGGCCCTCGTCTG 1635
Qy 574 TGCAGTCTCCCTGCGAGCCCGGGAGCGAAGAGACTGTGAAGGCATGCTTCTGCTG 633
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Db 2296 GCCAGAGGGGTGTCTCAAGTGGAGCATCTCGGATCTGTCTCTCATGGGTGCTGGGCTAC 2355
Qy 1294 AGCATGCTGTGATGGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1353
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RESULT 12

US-09-126-280-1

; Sequence 1, Application US/09126280

; Patent No. 6103524

; GENERAL INFORMATION:

; APPLICANT: Wu, Su

; APPLICANT: Belagaje, Rama M

; TITLE OF INVENTION: Metabotropic Glutamate Receptor Protein and Nucleic

; FILE OF INVENTION: Acid

; FILE REFERENCE: Sequence List

; Patent No. 6103524

; CURRENT APPLICATION NUMBER: US/09/126,280

; CURRENT FILING DATE: 1998-07-30

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 2670

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (13)..(2643)

US-09-126-280-1

Query Match 49.6%; Score 871; DB 3; Length 2670;

Best Local Similarity 72.1%; Pred. No. 1.7e-190;

Matches 1150; Conservative 0; Mismatches 436; Indels 9; Gaps 1;

Qy 43 GGGTTCGAGCCGATCTTCTCCAGCGCAGCGTGTGACACACAGCGCAACATCTGGTTT 102
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Qy 163 AGCCATCAAGAAAGTGTGCCAAACGAGAGCGCATCGGGCAGGATCTGGGCTATGAGCAG 222
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Qy 283 ATGACCGTGAACCTGTGTCGGCGCGTGAAGTCTCTGCTCGATGAGACCCCGTGGAT 342
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Db 1444 ACCAATGGAGTCCACAGAGTGGCGGGTACAGGCAAGTGGGCGAGTGGGAGAGACCTTC 1503
Qy 514 CACCTCAGAAATAGAGCGGATGAGTGGCCAGGAGTGGCCAGCAGCTGCCCGCTCCATC 573
Db 1504 AGACTGGATGTGGAGGCCCTGCAGTGGTCTGGCGACCCACAGAGTGGCCCTGCTCTG 1563
Qy 574 TGCAGTCTGCCCTGCACGCCCGGGAGCGAAAGACTGTGAAGGCACTGGCTGTGTC 633
Db 1564 TGCAGCTGCCCTGCGGGCCGGGAGCGGAGAGATGGTGAAGGGCGTCCCTGCTGT 1623
Qy 634 TGGCACTCGAGCCCTGCACCGGGTACCACTACCAAGTGGACCGCTACACCTGTAAAGAC 693
Db 1624 TGGCACTCGAGGCGCTGTGAACGGTACCGCTTCAGGTGGAGGATTTACATGCGAGGCC 1683
Qy 694 TGCCCTCAGCAGATCGGCGCCACAGAGAACCGCAGAGCTGCCAGCCCATCCCATCGTC 753
Db 1684 TGTCTGGGAGCATGAGGCCACGCGCCCAACACAGCGGCTGCGCGCCACACCTGTGTG 1743
Qy 754 AAGTTGGAGTGGGACTCGCGGTGGCGGTGTCGCCCTCTTCTGGCGCGTGGTGGGATC 813
Db 1744 CGCTGAGCTGTGCTCCCTCGGCGAGCGCGCGCTCTCTGCGCGCTGTGCGGATC 1803
Qy 814 GCGCGCAGCTGTTGCTGTGTGCTACGTTTGTGGCTACACGATACCGCCCATCGTCAAG 873
Db 1804 GTGGCCACTACACCGGTGTGGCCACCTTGTGGGTGAACAAACACGCCCATGTTCGG 1863
Qy 874 GCCTCGGCGCGGAACTGAGCTACGTGTGCTGGCGGCGATCTTTCTGTGTACGCCACT 933
Db 1864 GCCTCGGCGCGGAACTCACTACGTCTCTCTCACCGCATCTTCTCTATCTACGCCATC 1923
Qy 934 ACCTTCTCATGATGCGAGAGCGGACCTGTGGGACCTGTGCTCGCGCGCATCTTCTTA 993
Db 1924 ACCTTCTCATGTTGGCTGAGCTTGGGCGCGGCTGTGTGCGCGCGCAGGCTCTTCTCTG 1983
Qy 994 GGGCTCGGCATGAGCATCAGCTACGCGGCGCTGTGACCAAGACCAACCGCATTTACCGC 1053
Db 1984 GGCCTGGGACGACCCCTCAGCTACTCTGCTGCTGTCTACAAAGACCAACCGTATCTACCG 2043
Qy 1054 ATCTTTGACAGGGCAACGCTCGGTGAGTGGCGCGCTTTTCATCAGCGCCGCGCTCGAG 1113
Db 2044 ATCTTTGACAGGGCAAGGCTCGGTGACACCCCTCTCTCTCATCAGCCCCACCTCACAG 2103
Qy 1114 TGGCGCATCAGCTTCATCTCATCTCTCTGAGCTGTGCGGATCTGTGGTGTGGTGTG 1173
Db 2104 CTGTGTCATCAGCTTCAGCTCTCCTCGTGGAGTGTGGGATTAATTAACATGGTGGGG 2163
Qy 1174 GTGGACCCCTCCACTCGGTGTGATCTTCAGGACCAACGAGACTTTGACCCCGCTTT 1233
Db 2164 GCGCGGCCCCNACACAGCGTGTGATGATATAGGAAACAGCGACGCTGGACCCCGAGCAG 2223
Qy 1234 GCGAGGGCGTCTCAAGTGGACATCTCGGACCTGTCTCTCATCTGCTGCTGGGTAC 1293
Db 2224 GCGAGGGGTGCTCAAGTGGACATCTCGGATCTGTCTCTCATCGGCTGCTGGGTAC 2283
Qy 1294 AGCATGCTGTGATGCTGATGCTGTGTGATGCGCCATCAAGACCGAGGGGTGCGCGAG 1353
Db 2284 AGCTCTCTGCTCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCTGCTGCTGCTG 2343
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Qy 1354 ACCTTCAACGAGGCAAGCCCATGGCTTCAACATGTACACCACTGATGTCTGGCTG 1413
Db 2344 ACCTTCAACGAGGCAAGCCCATGGCTTCAACATGTACACCACTGATGTCTGGCTG 2403
Qy 1414 GCCTTCAATCCCATCTTTTGGCACTTCAAGTACAGTACAGGCAAGCTGTATATCCAGCA 1473
Db 2404 GCATTCGTGCCCATCTTTTGGCACTGCCAGTCACTGCTGAAAGATTTTATATCCAGCA 2463
Qy 1474 ACCACACTGACGGTCTCCGTGAGTCTGAGCGCTTTCAGTCTCCCTGGGATGCTCTACATG 1533
Db 2464 ACCAGCTAACGGTCTTTCAGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2523
Qy 1534 CCCAAGTCTACATCATCTCTTCCACCCGAGCAGAACGTCGCCAAGCGCAAGCGCAGT 1593
Db 2524 CCCAAAACCTAGTCTATCTTTTCCATCCAGAGCAGAAATGTGCAAGAGCGAAGCGGAGC 2583
Qy 1594 CTCAAGCCGTGTGTCACCGCGCCACCATGTCCNA 1628
Db 2584 CTCAAGGCCACCTCCACGCTGGCAGCCCCCNA 2618

RESULT 13
US-09-126-280-3
; Sequence 3, Application US/09126280
; Patent No. 6103524
; GENERAL INFORMATION:
; APPLICANT: Wu, Su
; APPLICANT: Belagaje, Rama M
; TITLE OF INVENTION: Metabotropic Glutamate Receptor Protein and Nucleic
; FILE OF INVENTION: Acid
; FILE REFERENCE: Sequence List
; Patent No. 6103524
; CURRENT APPLICATION NUMBER: US/09/126,280
; CURRENT FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2635
; TYPE: RNA
; ORGANISM: Human
US-09-126-280-3

Query Match 49.0%; Score 860.2; DB 3; Length 2635;
Best Local Similarity 57.7%; Pred. No. 5.2e-188;
Matches 945; Conservative 229; Mismatches 448; Indels 15; Gaps 3;

Qy 7 GGGGTATCATCATCTTTGGCCAAAGAGATGATC--AGGTTGACCGATCTTCTCCA 64
Db 974 GGGCAUCACCAUCUCCGCCAAAAGGGCCUCCACGACGGAUUGACGACUACUUAUGA 1033
Qy 65 GCGCACGCTGGACAAACAGCGGCAACATCTGTTTGGCGAGTCTTGGGAGGACAACT 124
Db 1034 CUCGAUCCCGUGAGAACACCGCAGGAACAUCUGGUGCGGAGUUCUGGGAAGAGAUAU 1093
Qy 125 TCCATTGCAAGTTTGAGCGCGCCACCGCTCAAGAAAGGAAGCCACATCAAGAAGTGCAC-- 182
Db 1094 UUAACUGCAACUGACAGCAGCUCAGUACCCAGUACAGAUUAUCCACCGCAAUUGCAG 1153
Qy 183 --CAACCGAGAGCGCATCGGGCAGGACTCGGCTATAGCAGGAGGAGGAGGAGTTC 240
Db 1154 GUCUACGAGGAACCAUCUGCGCGGACUCCACUACGAGCAGGAGGAGGAGGAGGAGU 1213
Qy 241 GTGATTACGCTGTGATGACGCTGCGGCGCAGCGCTGACGCGCATGACCGGTGACTGTGT 300
Db 1214 GUGAUAUGCGGUGAUGCAUUGCCCAAGCCUCCACAGCAUGACACGAGCGCUCUGC 1273
Qy 301 CCGCGCGCGTGGAGACTTGTCCCTCGCATGAGACCCCGTGGATGGCACCCAGCTGCTTAAG 360
Db 1274 CCUGGCGACACAGCGCUGUGCCCGCGAUGGAAACCCACCGAUGGGCGGAUUCUUGCAG 1333
Qy 361 TACATAGGAACGTCATCTTCTAGGCAATTTGCGGGGAAACCTGTAACTTCAATGAGAAC 420
Db 1334 UACAUCGAGGUGUCCGUCAUUGGCAAGCGCAGGAACCCCGUGUGAUCACGAGAAC 1393
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QY 421 GGAGAGCGACCGGGGCGCTACGACATCTACAGTACCACTGCGCAATGCGTCCGC----- 476
DB 1394 GGGGAUGCGCCCGGGCGGACGACAUUCUCCAGUACACCGCGCAACAAUGGCGAGUGCCAGC 1453
QY 477 -----CGAGTACAGGTCACTCGCTCGTGGACAGACCACTGCACCTCAGATAGAGCGG 531
DB 1454 AGUGGCGGUAACAGGACAGUGGGCCAGUGGGGAGAGACCUCAGACUGGAUGAGGAGGCC 1513
QY 532 ATGCACTGCGGAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCACTGCGCTGCGCTGCGCAG 591
DB 1514 CUGCAGUGGUCUGGCGACCCCAAGAGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1573
QY 592 CCGGGGAGCGAAGAGACTGTGAAGGCGATGGCTTGTGCTGGCACTGGAGCGCTGCG 651
DB 1574 CCGGGGAGCGAAGAGAGGUGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1633
QY 652 ACCGGGTACAGTACCAAGTGGACCGCTACACTGTGAAGCACTGCCCTACGACATGCGG 711
DB 1634 GAGGGUACCGUUCAGGUGGAGCAGUUAUACAGGAGCGGCGGCGGCGGCGGCGGCGG 1693
QY 712 CCCAGAGAGACCGCAGAGCTGCCAGCGCCATCCCATCGTCAAGTTGAGTGGGACTCG 771
DB 1694 CCCAGCGCAACACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1753
QY 772 CCGTGGCGGCTGCGCTCTTCTGCGGCTGGTGGGCACTGCGCGCGCAAGCTGTGCTG 831
DB 1754 CCGGCGGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1813
QY 832 GTGGTCACTGTTGCGCTACAGCATACCGCCATCGTCAAGCGCTCGGCGGCGGCACTG 891
DB 1814 GUGGCGACCGUUGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1873
QY 892 AGCTAGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 951
DB 1874 NACUACGUCUUCACCGCGCAUUCUUAUACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1933
QY 952 GAGCGGAGCCTGGGAGCTGTTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1011
DB 1934 GAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1993
QY 1012 AGCTAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1071
DB 1994 AGCUACUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2053
QY 1072 CCGTGGCTGAGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1131
DB 2054 CGCGGUGACACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2113
QY 1132 CTGATCTCCCTGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1191
DB 2114 CUCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2173
QY 1192 GTGGTGGACTTCAGGACCAAGGACACTTGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1251
DB 2174 GUGAUGACUAGAGGACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2233
QY 1252 TCGGACATCTCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311
DB 2234 UGCGACUUGCGAUGUUCUUAUAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2293
QY 1312 ACGTGTACTGTGACGCCATCAAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1371
DB 2294 ACGUGCACAGUGUAGCGCAUACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2353
QY 1372 CCCATGGGTTACCATGTGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1431
DB 2354 CCCAUGGCGUACCGCAUACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2413
QY 1432 TTGCGCACCTCAGTGCAGCGAGCTGTGATCTCAGACAAACACACTGACGCTGCTGCTGCTGCT 1491
DB 2414 UUGGCGACUGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2473

QY 1492 GTGAGTCTGAGCGCTTCACTGCTGCGGATGCTTACATGCCCAAGATCTACATCATC 1551
DB 2474 UUGAGCGUGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2533
QY 1552 CTCTTCCACCGCGGAGCAGAACTGCGCCAAAGCGGAGTCTCAAAGCGGCTGCTGCTGCTGCTGCT 1611
DB 2534 UUUUCCCAUCCAGCAGCAGAUUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2593
QY 1612 GCCGCCACCATGTCCAA 1628
DB 2594 GUGGAGCGGCCACCCAA 2610

RESULT 14
US-08-855-146-1
; Sequence 1, Application US/08855146
; Patent No. 6221609
; GENERAL INFORMATION:
; APPLICANT: Belagaje, Rama M.
; APPLICANT: Wu, Su
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Department
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,146
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,243
; FILING DATE: 07-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10836
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-6334
; TELEFAX: (317) 276-2764
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58..2781
US-08-855-146-1

Query Match 47.8%; Score 839; DB 3; Length 3321;
Best Local Similarity 68.6%; Pred. NO. 4.1e-183;
Matches 1173; Conservative 0; Mismatches 535; Indels 3; Gaps 1;

QY 43 GGGTTCGACCCATCTCTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 102
DB 1075 GGATTTGATGATGATCTTTAGAAAGCGGAACTCTTGCCAAATATCGAAGAAATGTGTGGTTT 1134
QY 103 GCCGAGTTCTGGGAGGACAACTTCATTGCAAGTTGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 162
DB 1135 GAGAAATCTGGAGGAGAAATTTGGCTGCAAGTTAGGATCAGATGGG---AAAAGGAAC 1191

QY 163 AGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGCGAGGAGCTCGGCTATGAGCAG 222
DB 1192 AGTCATATAAGAAATGACAGAGGCTGAGCGAATTGCTCGGATTCACTTATGACAG 1251
QY 223 GAGGGAAAGTGCAGTTCTGATTAAGACGCTGTGTAAGCCATGGGCCAGCGCTGCAGGCC 282
DB 1252 GAAGGAAAGTCCAAATTTGTAATGATGCTGTATATTCATGCTTCAATGCTTCAAGCTTCA 1311
QY 283 ATGACCGTGCAGCTGTGTCGCGCGCTGAGACTTGCCTTCGATGGACCCCGTGGAT 342
DB 1312 ATGACAAAGATCTCTGCGCTGGATACATTTGGCTTTGTCACGAATGAGTACCATGAT 1371
QY 343 GGCACCCAGCTGCTTAAGTATACATCAGGAACGTCACCTTCTCAGGCATTTGCGGGAAACCT 402
DB 1372 GGGAAAGAGCTACTTGGTTATATTCGGGCTGTAAATTTTATGGAGTGTCTGGCACTCT 1431
QY 403 GTAACTTTCAATGAGAACGGAGACGACCGGGGGCTACGACATCTACCAATGACCAACTG 462
DB 1432 GTCACTTTTAATGAAACGGAGATGCTCTCTGGAAGTTATGATATCTTCCAGTATCAATA 1491
QY 463 CGCAATGCTCGGCGGAGTACAGGTCTATCGCTCGTGACAGACCACTGCACCTCAGA 522
DB 1492 ACCRAAAAGACAGAGTACAAAGTCTATCGGCCATCGGACCAATCAAGCTTCACTTAAA 1551
QY 523 ATAGACGGATGCACTGCGGAGTGGCCAGAGCTGCGCGCTCGATCTGCAGTCTG 582
DB 1552 GTGGAGACATGCACTGGGCTCATAGAGACATCTACCGCGGCTGTGCTGAGCGCTG 1611
QY 583 CCCTGCCAGCCGGGAGCGAAGAACACTGTGAAGGGCATGGCTTGTCTGGCACTGC 642
DB 1612 CCGTGAAGCAGGGGAGGAGGAAGAAACGGTGAAGGGGTCCTTGTCTGGCACTGT 1671
QY 643 GAGCCTGCACGGGTACAGTACCAAGTGACCGCTACACTGTGAACCTGCCCTAC 702
DB 1672 GAACGCTGTGAAGGTTTAACTTACAGGTGATGAGCTGCTCTGTGAACCTTGGCCCTG 1731
QY 703 GACATGCGGCCACACAGAAACCGACAGCTGCCAGCCCATCCCATCGTCAAGTTGGAG 762
DB 1732 GATCAGAACCCACATGACCGGACAGCTGCCAGCTTATCCCATCATCAATTTGAG 1791
QY 763 TGGGATCGCGCTGGCGCTGTGCTCCCTCTTCCTGGCGGTGGGCAATCGCGCCACG 822
DB 1792 TGGCACTCTCCCTGGGCTGTGCTGCTGTGTTGTCATATTTGGGAATCATCGCCACC 1851
QY 823 CTGTTCTGGTGGTCACTGTTGTGGCTACACAGTACCCCATCGTCAAGGCTCGGC 882
DB 1852 ACCTTGTGATCGTGCACCTTTGTCCGCTATAATGACACACCTATGTTGAGGGCTCAG 1911
QY 883 CGGGAACCTGAGTACGTGCTGTCGGGGCATCTTCTGTGTCAGCGCACTACCTTCCTC 942
DB 1912 CGCGAACTTAGTTAGTCTCTTAACGGGGATTTTCTCTGTTATTCAATCAGTTTGA 1971
QY 943 ATGATCGCAGACCGGACCTGGGACCTGTTGCTCGCCCGCATCTTCTAGGGCTCGGC 1002
DB 1972 ATGATTCGAGCACGACATACATATGCTCTCTTCGAGCGGTCTTCTTAGGACTTGGC 2031
QY 1003 ATGACATCAGTACCGGCGCTGTGACGAGAACCAACCGATTTACGGCATCTTTGAG 1062
DB 2032 ATGTGTTTCAGCTATGACGCGCTTGTGACCAAAACAAACCGTATCCACGAATATTGAG 2091
QY 1063 CAGGCAAAACGTTGGTCACTGTCGCGGCTTTCATCAGCGCGGCTCGCAGCTGCGCATC 1122
DB 2092 CAGGGGAAGAATCTGTACAGCGCCCAAGTTTCAATGTCAGCATCTCAGCTGTGATC 2151
QY 1123 ACCTTCATCTCATCTCCCTCGAGCTGTGCGCATCTCGTGTGGTCTGTTGGTGAACCC 1182
DB 2152 ACCTTCAGCTCATCTCCGTCAGCTCTTGTGGAGTGTGTTGTGTTGTTGTGATCCC 2211
QY 1183 TCCCACTGGTGGTGCATCTCAGACCAACGGAACACTTGACCCCGCTTTGCCAGGGGC 1242
DB 2212 CCCCACATCATCTTGAATGAGGAGCGGACACTAGATCCACAGAAAGGCCAGGGGA 2271
QY 1243 GTGCTCAAGTGGACATCTCGGACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTG 1302

DB 2272 GTGCTCAAGTGTGACATTTCTGATCTCTCACTCATTTGTTCACTTGGATACAGTATCCTC 2331
QY 1303 CTGATGTCAGCTGTACTGTGTAGCCCATCAAGACCCGAGCGGTGCCGAGACCTTCAAC 1362
DB 2332 TTGATGTCATCTTGTACTGTTTATGCCAAATAAAACGAGAGGTGTCCGAGAGACTTCAAT 2391
QY 1363 GAGGCCAAGCCCATCGGCTTCCACATGTACACCACTTGCATTGTCTGGCTGGCCTTCATC 1422
DB 2392 GAAGCCAAACCTATTGGAATTTCCATGTATACCACTTGCATCATTTGGTTAGCTTTCATC 2451
QY 1423 CCATCTTTTTTGGSCACTCACAGTTCAGCCGACAAAGCTGTATCATCCAGAACCAACTG 1482
DB 2452 CCATCTTTTTTGGTCAGCCAGTTCAGCAAGAAAGATGTACATCCAGACAAACACTT 2511
QY 1483 ACGTCTCCGTGATCTGAGGCTTCACTGTCTCCCTGGGATGCTCTACATGCCCAAGTC 1542
DB 2512 ACTGCTCCATGATTTAAGTGTCTCATGTATCTCTGGGCACTCTATATGCCCAGGTT 2571
QY 1543 TACATCATCTCTTCCACCCGAGCAGAAAGTGCCTCAAGCGCAGCGCAGTCTCAAAGCC 1602
DB 2572 TATATTAATTTTTCATCCAGAACAGATGTTCAAAAACGCAAGAGGACTTCAAGCT 2631
QY 1603 GTGTCACCCGCGCCACCATGTCCAACAGTTTCAACAGTTTCAACAGAGGCACTTCAGGCCCAAT 1662
DB 2632 GTGTCAGAGCTGCCACCATGCAAGCAAACTGATCCAAAAGAAATGACAGACCAAT 2691
QY 1663 GGGGAACCCAAATCAGAGCTGTGTGAGAACTGTGAGACCCAGCGCTGGCTACCAACAG 1722
DB 2692 GCGAGGTGAAGTGAACCTCTGTGAGAGTCTTGAACCAACACTTCTCTACCAAGACA 2751
QY 1723 ACCTACGTCACCTACACCAACCATGCCATCT 1753
DB 2752 ACATATATCAGTTACGAATCATTCATCT 2782

RESULT 15

US-08-855-146-3
; Sequence 3, Application US/08855146
; Patent No. 6221609
; GENERAL INFORMATION:
; APPLICANT: Belagaje, Rama M.
; APPLICANT: Wu, Su
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Department
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,146
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,243
; FILING DATE: 07-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10836
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-6334
; TELEFAX: (317) 276-2764
; INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 3321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
US-08-855-146-3

Query Match 47.8%; Score 839; DB 3; Length 3321;
Best Local Similarity 52.5%; Pred. No. 4.1e-183;
Matches 898; Conservative 275; Mismatches 535; Indels 3; Gaps 1;
QY 43 GGGTTCACCGATCTTCTCCAGCGCGAGCTGAGCAACAACAGGCGCAACATCTGTTT 102
DB 1075 GGAUUGAUGCAUACUUAAGAACCGGAAACUCUUGGCAUAAUUGGAAUUGUGUGUU 1134
QY 103 GCGGAGTCTCGGAGGACAACTTCCATTGCAAGTTGAGCGCGACCGCTCAAGAGGA 162
DB 1135 GCAGAAUUCUGGAGGAGAAUUAUUGGUGCAAGUAGGAUACAUGGG---AAAGGAAC 1191
QY 163 AGCCACATCAAGAAGTGCACCAACCGAGAGCGCATCGGCGAGACTCGGCTTATGAGCAG 222
DB 1192 AGUCAUAUAAAGAACGACAGCGGUGGAGCGAAUUGCGGAUUAUUAUUGAACAG 1251
QY 223 GAGGGAAGGTGAGTTCGTGATGAGCGTGTGATGAGCATGGGCCAGCGCTGCAAGCC 282
DB 1252 GAAGGAAAGGUCAAUUAUUAUUGAUGUUAUUAUUGCAUGGUUUGCCUUGCCUGCAAU 1311
QY 283 ATGACCGTGTGCTGTCCCGCGCGGTAGGACTCTGCTCGCATGGACCGCCGTGAT 342
DB 1312 AUGCAAGAAGUUCUGGCCUGGAUACAUGGCCUUAUUGCCAGAAUGAGUACCAUUGAU 1371
QY 343 GGCACCCAGCTCTTAAGTACATCAGGAACGTCAACTTCTCAGGCAATGCGGGGAACCT 402
DB 1372 GGGAAAGAGCUACUUGUUAUUAUUGGCGUUAUUAUUGGAGUUGGCGACUCU 1431
QY 403 GTAACTTCAATAGAAACGAGACGCAACGGGCGGTAGCATCTACAGTACCAATG 462
DB 1432 GUCAUUAUUAUUAUUAUUAUUGGAGUUGGAGUUAUUAUUGGAGUUAUUAUUA 1491
QY 463 CGCAATGCTCGGCGAGTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522
DB 1492 ACCAACAAGACAGAGUACAAAGUACUGGCCACUGGACCAUACAGCUUUAUUA 1551
QY 523 ATAGAGCGGATCAGTGGCCAGGAGTGGCCAGAGCTGCCGCTCATCTGCACTGTG 582
DB 1552 GUGGAGACUAGUGGCGUUAUAGAGACAUACUACCCGCGGUGUUGGAGGAGG 1611
QY 583 CCTGCCAGCCCGGAGCGAAGAGACTGTGAAGGGGATGGTGTGCTGGCACTGC 642
DB 1612 CGUGUAGCCAGGCGAGAGGAGAAACCGUGAAGGGGUGCCUUGGUGGCGACUGU 1671
QY 643 GAGCCCTGCACCGGTACAGTACCAAGTGGACCGCTACACTGTAGACCTGCCCTTAC 702
DB 1672 GAACGUGUAGAGUUAACAACUACAGGUGGAGUAGUGUUGGAAUUAUUGCCUUG 1731
QY 703 GACATGCGGCCACAGAGAACCGCAGAGCTGCCAGGCCATCCCATCGTCAAGTTGGAG 762
DB 1732 GAUCAGAGACCCACAUAGAACCGCAGCGGUGCGAGCUUUAUCCCAUUAUUAUUGAG 1791
QY 763 TGGGACTCGCGTGGCGCGTGTGCTGCTTCTTCTGGCGGTGGGATCGCGCCACG 822
DB 1792 UGGCAUUCUCCUGGCGUGGUGGUGUUGUUAUUAUUGGAAUUAUUGGAAUUAUUGG 1851
QY 823 CTGTTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
DB 1852 ACCUUGUAGUGGAGACCUUUGUUGGCUAUAUUAUUAUUAUUAUUAUUAUUAUUA 1911
QY 883 CGGGAACGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 942
DB 1912 CCGGAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1971
QY 943 ATGATCGCAGAGCCGACCTGGGGACCTGTTGCTCGCTCGCGCGCATCTTCTTAGGGCTCGGC 1002

DB 1972 AUGAUGCAGCACCAGAUACAUAUUGCUCUCCGACGGGUCUUCUAGGACUUGGC 2031
QY 1003 ATGAGCATCAGTACGCGGCGCTGTGACCAAGACCAACCGCATTTATCCGCTCTTTGAG 1062
DB 2032 AUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2091
QY 1063 CAGGGAACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1122
DB 2092 CAGGGAAGAAUUAUUGUACAGAGCGCCCAAGUUAUUAUUAUUAUUAUUAUUAUUAUUA 2151
QY 1123 ACCTTTATCTCTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
DB 2152 ACCUUCAGCCUACUUCGCGUACUUCGUGAGUUAUUAUUAUUAUUAUUAUUAUUAUUA 2211
QY 1183 TCCCACTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1242
DB 2212 CCCCAUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2271
QY 1243 GTGCTCAAGTGGGACATCTCGGACCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1302
DB 2272 GUGCUAAGUGUACAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2331
QY 1303 CTGATGTCAGT 1362
DB 2332 UUGAUGGUCACUUGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2391
QY 1363 GAGGCAAGCCATCGGCTTCAACATGTACACCATGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1422
DB 2392 GAGGCAAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2451
QY 1423 CCCATCTTTTGGCACCTCAGTTCAGCGACGAGTGTGTATCATCCAGACCAACCACTG 1482
DB 2452 CCCAUUUUUUUGUACAGCCAGUCAGCAGAGAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUA 2511
QY 1483 ACCTGCTCCGTGAGTCTGAGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1542
DB 2512 ACUGUCUUAUGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2571
QY 1543 TACATCATCTCTTCCACCCGAGCAGAACTGCGCCAGCGCAGCGAGTCTCAAAGCC 1602
DB 2572 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2631
QY 1603 GTGCTCAACCGCGCCACCATGTCCAAAGTTTCAACAGAGGGGCAACTTCAGGCCCAAT 1662
DB 2632 GUGGUGACAGCUGCCACCAUGCAAAAGCAACUGAUCCAAAAGGAAUUAUUAUUAUUAUUA 2691
QY 1663 GGGGAGCCAAATCAGAGCTGTGTGAGAACTGTGAGACCCCGAGCGCTGGCTACCAACAG 1722
DB 2692 GCGGAGGUGAAGAGUAAACUCUGUGAGAGUCUUGAAGCAACACUUCUUAUUAUUAUUA 2751
QY 1723 ACCTAGCTCACTACACCAACCATGCTCATCT 1753
DB 2752 ACAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2782

Search completed: June 21, 2005, 08:56:07
Job time : 319 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 01:52:20 ; Search time 983 Seconds
(without alignments)
10568.816 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 1755

Sequence: 1 atgcacggggatcatcatc.....acacacacatgcacatctag 1755

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1755	100.0	1755	8	ACC70676 Rat gluta
2	1707.6	97.3	2838	8	ABX16077 Rat CDNA
3	1473.8	84.0	2694	12	ADO29096 Mouse nov
4	1470.8	83.8	2739	12	ADO29776 Human nov
5	1470.8	83.8	3431	6	AAD38025 Human met
6	1470.8	83.8	3431	6	AAD38024 Human met
7	1470.8	83.8	3884	8	ABX16087 Human cDN
8	1470.8	83.8	3884	8	ABZ42692 Human met
9	1470.8	83.8	3884	10	ADE07285 Novel cod
10	1470.8	83.8	3884	10	ACA56476 Human sig
11	1470.8	83.8	3884	12	ADI56272 Human pol
12	1470.8	83.8	3884	13	AQO89113 Human uro
13	1469.2	83.7	3880	2	AAT03888 Human mgl
14	1468.2	83.7	2738	2	AAQ89342 Human mgl
15	1422.8	81.1	3470	13	ADR06667 Full leng
16	1340.6	76.4	3590	13	ADR10413 Full leng
17	1337.8	76.2	4271	13	ACN43319 Human dia
18	1311.2	74.7	4342	13	ACN43318 Human dia
19	880.6	50.2	2634	12	ADO29778 Human nov
20	880.6	50.2	2961	2	AAT38322 Metabotro

21	880.6	50.2	5560	6	AAS98044 Human DNA
22	880.6	50.2	6122	8	ABZ42694 Human met
23	880.6	50.2	6122	13	ADR14184 Human NF-
24	871	49.6	2670	3	AAA59554 DNA encod
25	860.2	49.0	2635	3	AAA59555 RNA encod
26	851.8	48.5	2727	12	ADO30247 Mouse GPC
27	851.8	48.5	2830	6	AAI72375 mGluR8 ge
28	851.8	48.5	2830	8	ABX11190 Murine me
29	840.6	47.9	2727	9	ACF05181 Human mgl
30	840.6	47.9	2727	9	ACF05180 Human met
31	839	47.8	2727	6	ABQ72799 Human GRM
32	839	47.8	2727	9	ACF05182 Human GRM
33	839	47.8	2727	9	ACF05183 Human mgl
34	839	47.8	2727	12	ADO29957 Human GPC
35	839	47.8	3321	2	AAV04206 Human met
36	839	47.8	3321	2	AAV04207 Human met
37	839	47.8	3321	8	ABZ42696 Human met
38	839	47.8	3321	10	ADE31728 Human 255
39	839	47.8	3321	13	ADO89127 Human uro
40	826.8	47.1	2613	12	ADO29102 Mouse nov
41	825.4	47.0	3280	5	AAS93639 DNA encod
42	823.8	46.9	3833	2	AAV17116 Metabotro
43	821.6	46.8	2997	2	AAQ99209 Rat metab
44	821.6	46.8	3417	8	AAD48709 Rat metab
45	819.6	46.7	2745	12	ADO29105 Mouse nov

ALIGNMENTS

RESULT 1
ACC70676
ID ACC70676 standard; DNA; 1755 BP.
XX
AC ACC70676;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rat glutamic acid receptor coding sequence.
XX
KW Rat; anorectic; antiulcer; antidiabetic; laxative; antidiarrhetic;
KW glutamic acid receptor; receptor; gastrointestinal tract disorder;
KW sitteirgia; obesity; ulcer; diabetes; constipation; diarrhoea; gene; ds.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 1..1755
FT /tag= a
FT /product= "Glutamic acid receptor"
XX
XX WO2003035873-A1.
XX
PD 01-MAY-2003.
XX
PF 23-OCT-2002; 2002WO-JP010984.
XX
PR 23-OCT-2001; 2001JP-00325159.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI San Gabriel A, Maekawa T, Uneyama H, Torii K;
XX
DR WPI; 2003-430418/40.
XX
P-PSDB; ABR56244.
XX
PT Novel glutamic acid receptor protein and encoded DNA, applicable in
PT screening agonists or antagonists of glutamic acid or allosteric
PT modulator for use as drugs in ameliorating symptoms and diseases e.g.
XX obesity.
XX Example 1; Page 30-33; 39pp; Japanese.
XX

CC The present sequence is the coding sequence for rat glutamic acid
CC receptor. The receptor has a transmembrane domain and an intracellular
CC domain common to type 4 metabotropic glutamic acid receptor protein, and
CC an extracellular domain shorter by 316 or 327 amino acid residues than
CC type 4 metabotropic glutamic acid receptor protein. The receptor and its
CC coding sequence are useful in screening agonists or antagonists of
CC glutamic acid or allosteric modulator for use as drugs in ameliorating
CC symptoms and diseases due to abnormal metabolism in gastrointestinal
CC tract including small and large intestines e.g. sitielirgia, obesity,
CC ulcer, diabetes, constipation and diarrhoea
XX

SQ Sequence 1755 BP; 364 A; 581 C; 479 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 1755; DB 8; Length 1755;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGCGAGGGGTATCATCATCTTTGCAACGAGGATGACATCAGGGTTCGACCGATCTTC 60
DB 1 ATGCGAGGGGTATCATCATCTTTGCAACGAGGATGACATCAGGGTTCGACCGATCTTC 60
QY 61 TCCAGCCGACGCTGGACAAACAGAGGCGCAACATCTGTTTCCGAGTTCTGGAGGAC 120
DB 61 TCCAGCCGACGCTGGACAAACAGAGGCGCAACATCTGTTTCCGAGTTCTGGAGGAC 120
QY 121 AACTTCCATTGCAAGTTGAGCGCGCCACCGCTCAAGAGGGAAGCCACATCAAGAGTGC 180
DB 121 AACTTCCATTGCAAGTTGAGCGCGCCACCGCTCAAGAGGGAAGCCACATCAAGAGTGC 180
QY 181 ACCAACCGAGAGCGCATCGGCGAGGACTCGGCTATGAGCAGGAGGGAAGTGCAGTTC 240
DB 181 ACCAACCGAGAGCGCATCGGCGAGGACTCGGCTATGAGCAGGAGGGAAGTGCAGTTC 240
QY 241 GTGATTGAGCTGTGTAGCGCATGGGCCACCGGCTGCAAGCCATGCAACGCTGTGTGT 300
DB 241 GTGATTGAGCTGTGTAGCGCATGGGCCACCGGCTGCAAGCCATGCAACGCTGTGTGT 300
QY 301 CCGCGCGGTAGGACTTGCCTCGCATGGACCCCGGTGGATGGACCCAGCTGCTTAAG 360
DB 301 CCGCGCGGTAGGACTTGCCTCGCATGGACCCCGGTGGATGGACCCAGCTGCTTAAG 360
QY 361 TACATCAGGAACGTCAACTTCTCAGGCAATGCGGGGAACCCCTGTAACTTCAATGAGAAC 420
DB 361 TACATCAGGAACGTCAACTTCTCAGGCAATGCGGGGAACCCCTGTAACTTCAATGAGAAC 420
QY 421 GGAGACGACCGGGCGGTACGACATCTACAGTACCAACTGCGCAATGGCTCGGCGAG 480
DB 421 GGAGACGACCGGGCGGTACGACATCTACAGTACCAACTGCGCAATGGCTCGGCGAG 480
QY 481 TACAGGTCATCGGCTCGTGGACAGACCACTGCACTCAGAAATAGAGCGGATGCAAGTGG 540
DB 481 TACAGGTCATCGGCTCGTGGACAGACCACTGCACTCAGAAATAGAGCGGATGCAAGTGG 540
QY 541 CCAGGGAGTGGCAGCAGCTGCGCGCTCCATCTGCACTCTGCCCTGCGAGCCCGGGGAG 600
DB 541 CCAGGGAGTGGCAGCAGCTGCGCGCTCCATCTGCACTCTGCCCTGCGAGCCCGGGGAG 600
QY 601 CGAAGAAGACTGTGAAGGCAATGGCTGTGCTGGCACTGGAGCCCTGCAACGGGATAC 660
DB 601 CGAAGAAGACTGTGAAGGCAATGGCTGTGCTGGCACTGGAGCCCTGCAACGGGATAC 660
QY 661 CAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTTACGACATGGGCGCCACAGAG 720
DB 661 CAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTTACGACATGGGCGCCACAGAG 720
QY 721 AACCGCAGAGCTGCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGGCC 780
DB 721 AACCGCAGAGCTGCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGGCC 780
QY 781 GTGCTGCCCTTCTTCTGCGCGGTGGGCAATCGCGCCACGCTGTTGTGGTGTACAG 840
DB 781 GTGCTGCCCTTCTTCTGCGCGGTGGGCAATCGCGCGCATCGCGCCACGCTGTTGTGGTGTACAG 840
```

RESULT 2

ABX16077

ID ABX16077 standard; cDNA; 2838 BP.

XX ABX16077;

AC ABX16077;

XX 03-APR-2003 (first entry)

DT

XX

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QY 841 TTTGTGCGCTACAAAGATACCCCATCGTCAAGGCTCTGGGCGGGAACTGAGCTACGTG 900
DB 841 TTTGTGCGCTACAAAGATACCCCATCGTCAAGGCTCTGGGCGGGAACTGAGCTACGTG 900
QY 901 CTGCTGCGGGGCACTTTTCTGTGTAGCGCACTACCTTCTCATGATCGAGAGCGGAC 960
DB 901 CTGCTGCGGGGCACTTTTCTGTGTAGCGCACTACCTTCTCATGATCGAGAGCGGAC 960
QY 961 CTGGGGACCTGTTTCGCTCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGTACGCG 1020
DB 961 CTGGGGACCTGTTTCGCTCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGTACGCG 1020
QY 1021 GCCCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGGCAACGCTCGGTC 1080
DB 1021 GCCCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGGCAACGCTCGGTC 1080
QY 1081 AGTCCCGCGGTTTTCATCAGCCGCGCTCGCAGCTGCGCCATCACCTTTCATCTCTCC 1140
DB 1081 AGTCCCGCGGTTTTCATCAGCCGCGCTCGCAGCTGCGCCATCACCTTTCATCTCTCC 1140
QY 1141 CTGCAGCTGCTCGGCATCTGCGTGTGTGTGCTGAGGAGCCCTCCCACTCGGTGGTGCAC 1200
DB 1141 CTGCAGCTGCTCGGCATCTGCGTGTGTGTGCTGAGGAGCCCTCCCACTCGGTGGTGCAC 1200
QY 1201 TTCCAGAGCAACCAAGCACTTTGACCCCGCTTTTGCCAGGGCGGTGCTCAAGTGCAGATC 1260
DB 1201 TTCCAGAGCAACCAAGCACTTTGACCCCGCTTTTGCCAGGGCGGTGCTCAAGTGCAGATC 1260
QY 1261 TCGAGCTGTCTCTCATCTGCTGTGGGTACAGCATGTCTGTGATGGTCACTGTACT 1320
DB 1261 TCGAGCTGTCTCTCATCTGCTGTGGGTACAGCATGTCTGTGATGGTCACTGTACT 1320
QY 1321 GTGTACCGCATCAAGACCCGAGGGTCCCGAGACCTTCAACGAGGGCAAGCCCATCGGC 1380
DB 1321 GTGTACCGCATCAAGACCCGAGGGTCCCGAGACCTTCAACGAGGGCAAGCCCATCGGC 1380
QY 1381 TTCAACATGTACACCACTGCTGCTGTGGCTTTCATCCCATCTTTTGTGGCAAC 1440
DB 1381 TTCAACATGTACACCACTGCTGCTGTGGCTTTCATCCCATCTTTTGTGGCAAC 1440
QY 1441 TCACAGTCAGCCGCAAGCTGTATCATCCAGAAACCACTGACGGTCTCGGTGAGTCTG 1500
DB 1441 TCACAGTCAGCCGCAAGCTGTATCATCCAGAAACCACTGACGGTCTCGGTGAGTCTG 1500
QY 1501 AGCGCTTCAGTGTCCCTGGGGATGCTCTACATGCCCAAGTCTACATCATCTCTCCAC 1560
DB 1501 AGCGCTTCAGTGTCCCTGGGGATGCTCTACATGCCCAAGTCTACATCATCTCTCCAC 1560
QY 1561 CCGGAGCAGAAACGTCGCCAAGCGCAAGCGAGTCTCAAAGCCGTGGTCAACGCCCAAC 1620
DB 1561 CCGGAGCAGAAACGTCGCCAAGCGCAAGCGAGTCTCAAAGCCGTGGTCAACGCCCAAC 1620
QY 1621 ATGTCCAAAGTTTACACAGAGGGCAATTTCAGGCCCCAATGGGGAGGCCAAATCAGAG 1680
DB 1621 ATGTCCAAAGTTTACACAGAGGGCAATTTCAGGCCCCAATGGGGAGGCCAAATCAGAG 1680
QY 1681 CTGTGTGAGACCTTGGAGACCCCGAGCGCTGGCTACCAACAGACCTTACCTACAC 1740
DB 1681 CTGTGTGAGACCTTGGAGACCCCGAGCGCTGGCTACCAACAGACCTTACCTACAC 1740
QY 1741 AACCATGCCATCTAG 1755
DB 1741 AACCATGCCATCTAG 1755
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Db 1490 GCTGATGTCACGTCTACTGTGTGTCAGCCATCAAGACCCGAGCGGTGCGGAGACCTTCAA 1549
Qy 1362 CGAGGCCAAGCCATCGGCTTACCATGTACACCACTGCAATTCGTGCTGGCTGGCTTCAT 1421
Db 1550 CGAGGCCAAGCCATCGGCTTACCATGTACACCACTGCAATTCGTGCTGGCTGGCTTCAT 1609
Qy 1422 CCCCATCTTTTGGCACTCACAGTCAGCGCAGCAGCAAGCTGTACATCCACAGACCAACACACT 1481
Db 1610 CCCCATCTTTTGGCACTCACAGTCAGCGCAGCAGCAAGCTGTACATCCACAGACCAACACT 1669
Qy 1482 GACGCTCTCCGTAGTCTGAGCGCTTTCAGTGTCCCTGGGGATGCTCTACATGCCCAAGT 1541
Db 1670 GACTGTCTCCGTAGTCTGAGCGCTTTCAGTGTCCCTGGGGATGCTCTACATGCCCAAGT 1729
Qy 1542 CTACATCATCTCTTCCACCGGAGCAGAAAGTGTCCCAAGCGCAGCCAGCTCTCAAGC 1601
Db 1730 CTACATCATCTCTTCCACCGGAGCAGAAAGTGTCCCAAGCGCAGCCAGCTCTCAAGC 1789
Qy 1602 CGTGTCTACCGCGCCACCATGTCCCAAGTTCACAGAGGCGCACTTCAGGCCCAA 1661
Db 1790 CGTGTCTACCGCGCCACCATGTCCCAAGTTCACAGAGGCGCACTTCAGGCCCAA 1849
Qy 1662 TGGGAAGCCAAATCAGAGCTGTGTGAGAACCTGGAGACCCCGCTGGCTTACCAACA 1721
Db 1850 TGGGAAGCCAAATCAGAGCTGTGTGAGAACCTGGAGACCCCGCTGGCTTACCAACA 1909
Qy 1722 GACCTACGTACCTACACCAACCATGCCATCTAG 1755
Db 1910 GACCTACGTACCTACACCAACCATGCCATCTAG 1943

RESULT 3

ID ADO29096
AC ADO29096
DT 29-JUL-2004 (first entry)
XX Mouse novel GPCR GRM4 polynucleotide, SEQ ID NO:195.
DE G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cystostatic; antiinflammatory; vasotropic; antidiagonal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW viricide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
KW murine; gene; ss.

OS Mus musculus.

XX WO2004040000-A2.

PN 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

PF 09-SEP-2003; 2002US-0409303P.

PR 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

PA Gaitanaris GA, Bergmann JE, Gragorov A, Hohmann J, Li F;

XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.
DR P-PSDB; ADO29095.
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX Claim 13; SEQ ID NO 195; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancer). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2694 BP; 544 A; 866 C; 757 G; 527 T; 0 U; 0 Other;

Qy Query Match 84.0%; Score 1473.8; DB 12; Length 2694;
Db Best Local Similarity 92.2%; Pred. No. 2.8e-308; Mismatches 1578; Conservative 0; Indels 36; Gaps 1;
Qy 42 AGGTTTCGACCGATATCTTCCAGCCGACGCTGGACAAACAGCGGCAACATCTGGTT 101
Db 1020 AGGTTTCGACCGATATCTTCCAGCCGACGCTGGACAAACAGCGGCAACATCTGGTT 1079
Qy 102 TGCCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCGGCCACGCGCTCAAGAGGG 161
Db 1080 TGCTGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCGGCCACGCGCTCAAGAGGG 1139
Qy 162 AAGCCACATCAGAGAGTGCACCACGAGCGCATCGGCGAGGACTCGGCGCTATGAGCA 221
Db 1140 AAGCCACATCAGAGAGTGCACCACGAGCGCATCGGCGAGGACTCGGCGCTATGAGCA 1199
Qy 222 GGAGGGGAAGGTGCAGTTTCGTGATTGACGCTGTGTAGCCATGGGCCACCGCTGCACGC 281
Db 1200 GGAGGGGAAGGTGCAGTTTCGTGATTGACGCTGTGTAGCCATGGGCCATGCTTCGACGC 1259
Qy 282 CATGACCCGTAACCTGTGTCGCCGCCGTAGGACTCTGCCCTCGCATGGAACCCCGTGA 341
Db 1260 CATGACCTGTGACCTGTGTCGCCGCCGTAGGACTCTGCCCTCGCATGGAACCCCGTGA 1319
Qy 342 TGGCACCACGCTGCTTAAGTACATCAGAGAGTCAACTCTTCAGGSCATTCGGGGGAACCC 401
Db 1320 TGGCACCACGCTGCTTAAGTACATCAGAGAGTCAACTCTTCAGGSCATTCGGGGGAACCC 1379

Qy	402	TGTAACCTTCAATGAGAACGGAGACGACCGGGGGCTGTACGACATCTACCAATGACCAACT	461
Db	1380	GGTGACCTTCAACGAGAACCGGAGACGGCCACGGGCGTTATGACATCTACCAAGTACCAACG	1439
Qy	462	GCGCAATGGCTTCGGCCGAGTACAAGGTCAATCGGCTCGTGGACAGACCACTTGACACCTCAG	521
Db	1440	TCGGCAACGGCTTCGGCTGAGTACAAGGTCAATCGGCTCAATGACAGACCACTTGACACCTCAG	1499
Qy	522	AATAGAGCGGATGTCAGTGGCGAGGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT	581
Db	1500	A-----CTGCCAGCTCCATCTGCAGCCT	1523
Qy	582	GCCCTGCAGCCCGGGAGCGAAGAAGACTGTGAAGGGCATGGCTTGTCTGTGGCACTG	641
Db	1524	GCCCTGCAGCAGCGAGCGGAAGAAGACGGTGAAGGGCATGGCTTGTCTGTGGCACTG	1583
Qy	642	CGAGCCCTGCACCGGGTACCAGTACCAAGTGGAGCGCTACACCTGTAAAGACCTGCCCCCTA	701
Db	1584	CGAGCCCTGCACCGGGTACCAGTACCAAGTGGAGCGCTACACCTGTAAAGACCTGCCCCCTA	1643
Qy	702	CGACATCGGCCCCACAGAGAACCCAGCAGCTGCGACGCCCATCCCCATCGTCAAGTTGGA	761
Db	1644	TGACATGGGCCCCACGGAAGAACCGCAGAGCTGCAGGCCCATACCCATTTGTCAGTTGGA	1703
Qy	762	GTGGGACTCGCCGTGGGGCGTGTGCCCCCTTCTCGCCGCGTGTGTGGGCATTCGCGCGCAC	821
Db	1704	GTGGGACTCACCTTGGGCTGTGTGCCCCCTTCTCGTGGCTGTGTGGGCATTTGTGCGCAC	1763
Qy	822	GCTGTTCTGGTGGTCAAGTTGTGCGCTACACGATACCCCCATCGTCAAGCGCTCGG	881
Db	1764	GCTGTTCTGGTGGTCACTTTGTGTCGTACAACGACACTCCGATCGTCAAGGCGCTCGG	1823
Qy	882	CCGGGAACCTGAGCTACGTGCTGTGGGGGGCATCTTTCTGTGCTACGCCACTACCTTTCCT	941
Db	1824	CCGGGAGCTGAGCTACGTCTGTGTGGGGGCACTTTTCTCTGTATGCGACCACTTTCCT	1883
Qy	942	CATGATCGCAAGCGGACCTTGGGGAAGCTGTTGCTCCGCGGCATCTTCTAGGGCTCGG	1001
Db	1884	CATGATCGCAGAGCTGACCTGGGAGCTGTTTCACTCCGCGGCATCTTCTGGGGCTTGG	1943
Qy	1002	CATGAGATCAGCTACGGGGCCCTGTGACCAAGACCAAACGGCATTTACCGCATCTTTGA	1061
Db	1944	CATGAGCATCAGCTACCGGCCCTGTCTGCAACAGCAACCGCATCTACCGCATCTTTGA	2003
Qy	1062	GCAGGCAAAAGGTTCAGTGCAGTCCCGCGCTTTCATCAGCCCGGCTTCGAGCTGGCCAT	1121
Db	2004	GCAGGCAAGGGTTCAGTGCAGTCCCGGCCCATCGGTTTCATCAGCCCGCTTCGAGCTGGCCAT	2063
Qy	1122	CACCTTCATCCTCATCTCCCTGCAGCTGCTCGGCATCTGGGTGTGGTTCTGTGGGACCC	1181
Db	2064	CACCTTCCTCATCTCGTGCAGTTGCTTGGCATCTGCGTGTGGTTCTGTGGGACCC	2123
Qy	1182	CTCCACTCGGTGTGACTTCAGGACCAAACGAGACATTTGACCCCGCTTTTGGCAGGG	1241
Db	2124	CTCCACTCGGTGTGACTTCCAGGACCAACGAGACACTTGAACCCCGCTTCGCGCGGGG	2183
Qy	1242	CGTGCTCAAGTGCACATCTCGGACCTGCTCCCTCATCTGCTGCTGGGCTACAGCATGCT	1301
Db	2184	TGTGCTCAAGTGTGACATCTCGGACCTGCTGCTCATCTGCTCTCTGGGCTACAGCATGCT	2243
Qy	1302	GCTGATGGTCAAGTGTGATCGGCATCAAGACCCGAGGGGTGCCCGAGACCTTCAA	1361
Db	2244	GCTGATGGTCAAGTGTGATCGGCATCAAGACCTCAAGACCTCGAGGGGTGCCCGAGACCTTCAA	2303
Qy	1362	CGAGGCCAAGCCATCGGCTTACCATGTATACCACTGCAATGTCTGGCTGGGCTTTCAT	1421
Db	2304	CGAGGCCAAGCCATCGGCTTACCATGTATACCACTGCAATGTCTGGCTGGGCTTTCAT	2363
Qy	1422	CCCCATCTTTTGGGCACTTCAGTGCAGCGGCAAGCTGTACATTCAGACACCACT	1481
Db	2364	CCCCATCTTTTGGGCACTTCAGTGCAGCGGCTGCAAGCTGTACATTCAGACACCACT	2423
Qy	1482	GACGGTCTCGGTGAGTCTGAGCGCTTTCAGTGTCCCTGGGAGTGTCTACATATGCCAAAGT	1541

(GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct_sequences](http://wipo.int/pub/published/pct_sequences).

Sequence 2739 BP; 545 A; 888 C; 783 G; 523 T; 0 U; 0 Other; XX

Query Match 83.8%; Score 1470.8; DB 12; Length 2739;
Best Local Similarity 91.1%; Pred.No. 1.3e-307;
Matches 1562; Conservative 0; Mismatches 152; Indels 0;

Qy	42	AGGTTTCGACCGATATCTTCTCCAGCCGACGCTGGACAAACAAGGCGCAACATCTGGTT	101
Db			
	1026	AGGCTTCGACCGCTACTTCTCCAGCCGACGCTGGACAAACAACGGGCGCAACATCTGGTT	1085
Qy	102	TGCCGAGTTCTGGGAGAGACAACCTTCCATTGCAAGTTGAGCGGCCACGGCTCAAGAGGG	161
Db			
	1086	TGCCGAGTTCTGGGAGAGACAACCTTCCACTGCAAGCTGAGCGGCCACGCCCTCAAGAGGG	1145
Qy	162	AAGCCACATCAAGAAGTGCCAAACAGAGAGCGATCGGCGAGGACTCGCGCTTATGAGCA	221
Db			
	1146	CAGCCACGTCAAGAAGTGGCAACACCGTAGCGAATTTGGGAGGATTCAGCTTATGAGCA	1205
Qy	222	GGGGGGAAGGTGACGTTTCGTGATTGACGCTGTGTAGCCATGGGCCACGCGCTGCACGC	281
Db			
	1206	GGGGGGAAGGTGACGTTTGTGATCGATCCGTGTACGCCATGGGCCACGGCTGCACGC	1265
Qy	282	CATGCAACGTCGACTGTGTCCCGGCCGCTAGGACTCTGCGCTTGCATTGACCCCGTGGGA	341
Db			
	1266	CATGCAACGTCGACTGTGTCCCGGCCGCTGGGGCTCTGCGCGCATGGAACCTGTAGA	1325
Qy	342	TGGCACCCAGCTGCTTAAGTATACATCAGGAAGCTCAACTTCTCAGGCATTCGGGGACCC	401
Db			
	1326	TGGCACCCAGCTGCTTAAGTATACATCCGANAACGTCAACTTCTCAGGCCATCGAGGAAACC	1385
Qy	402	TGTAACCTTCAATCAGAACGAGAGCGACCGGGCGCTACGACATCTACAGATACCAACT	461
Db			
	1386	TGTGACCTTCAATGAGAAATGGAGATGGCCCTGGGCGCTATGACATCTACCAATACCAGCT	1445
Qy	462	GCGCAATGGCTCGGCCGAGTACAAGGTCAATGGCTCTGGACTGACCACTGACACCTTAG	521
Db			
	1446	GCGCAACGATTCGCCGAGTACAAGGTCAATGGCTCTGGACTGACCACTGACACCTTAG	1505
Qy	522	AATAGACGGATGCAATGGCCAGGAGTGGCCAGCAGCTGCCGCGCTCCATCTGCAGTCT	581
Db			
	1506	AATAGACGGATGCACTGGCCGGGAGCGGAGCAGCTGCCGCGTCCATCTGCAGCT	1565

Db 2646 CGGAGAGGCAAGTCTGAGCTTGGAGAACTTGGAGGCCCGGCGCTGCGCACCAACA 2705
QY 1722 GACCTACGTCACCTACCAACCAACGACCTAG 1755
Db 2706 GACTTACGTCACCTACCAACCAACGACCTAG 2739

RESULT 5

AAAD38025
ID AAD38025 standard; RNA; 3431 BP.

XX AAD38025;
XX 10-SEP-2002 (first entry)
XX Human metabotropic glutamate (mGluR4) receptor RNA.
XX Human; metabotropic glutamate receptor; mGluR4; neurodegeneration;
KW antipsychotic; anticonvulsant; analgesic; antidepressant; antiemetic;
KW gene; ss.
XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 26..2764
FT /*tag= a
FT /product= "Human metabotropic glutamate receptor"

XX US6384205-B1.
XX 07-MAY-2002.
XX 18-AUG-2000; 2000US-00641318.
XX 12-MAR-1996; 96US-0013189P.
XX 12-MAR-1997; 97US-0081617B.
XX (ELIL) LILLY & CO ELI.
XX Belagaje RM, Wu S;
XX WPI; 2002-442818/47.
XX P-PSDB; AAE23757.

XX New nucleic acid encoding human metabotropic glutamate receptor, useful
PT e.g. in screening for specific agonists and antagonists for treating e.g.
PT neurodegeneration.

PS Claim 1; Col 23-26; 35pp; English.

XX The present invention relates to human metabotropic glutamate receptor
CC (mGluR4) proteins and polynucleotides encoding such proteins. Mglur4
CC sequences of the invention are useful for treating acute and chronic
CC neurodegeneration. They are also used as antipsychotic, anticonvulsant,
CC analgesic, antidepressant and antiemetic agents. They are also useful for
CC the diagnosis and/or treatment of conditions associated with an excess or
CC deficiency of mGluR4. The present sequence is human mGluR4 RNA

XX Sequence 3431 BP; 648 A; 1128 C; 949 G; 0 T; 706 U; 0 Other;

Query Match 83.8%; Score 1470.8; DB 6; Length 3431;
Best Local Similarity 74.2%; Pred. No. 1.3e-307;
Matches 1271; Conservative 291; Mismatches 152; Indels 0; Gaps 0;

QY 42 AGGTTGACCAATCTCTCAGCGCGACGCTGACAAACAGCGCGCAATCTGTT 101
Db 1051 AGGCUCCAGCCGACUUCUCCAGCGCGACGCGGACAAACCGCGCGCAACUCCG 1110
QY 102 TCCGAGTCTCGGAGGACAACTTCATTGCAAGTTGAGCGCGCGCTCAAGAGG 161
Db 1111 UGCCGAGUUCUGGGAGGAACUUCUCCAGGAGGCGCGCGCGCGCGCGCGCGCG 1170

QY 162 AAGCCACATCAAGAGTGTCACCAACGAGAGCGGCATCGGGCAGGACTCGGCCATGAGCA 221
Db 1171 CAGCCACGUCACGAGAGUGACCAACCGUGAGAGAAUUGGGCAGGAAUUCAGCUUAGAGCA 1230
QY 222 GGAGGGGAAGGTGCAAGTTCGTGATGAGCGCTGTGTACGCCATGGGCCACGCGCTGACGC 281
Db 1231 GGAGGGGAAGGUGGCGUUGUUGAUCGAGUGCCGUGUACGCCAUGGGCCACGCGUGCAGCG 1290
QY 282 CATGACCCGTGACCTGTGTCCCGCGCGGTAGGACTCTGCCCTCGCATGGACCCCGTGA 341
Db 1291 CAUGCACCGUGACCGUGUCCCGCGCGGUGGGGUCUGCCGCGCAUGGACCCUGUAGA 1350
QY 342 TGGCACCCAGCTGTAAAGTACATCAGGAACGTCACCTTCTCAGGCAATTCGGGGACCC 401
Db 1351 UGGCACCCAGCTGTAAAGTACATCAGGAACGTCACCTTCTCAGGCAATTCGGGGACCC 1410
QY 402 TGTAACTTCAATGAGAACGAGACGACCGCGGGCGCTACGACATCTACAGTACCAACT 461
Db 1411 UUGGACCUUCAAUGAAGUAGGAGUGCCGUGGGGCUAUGACUACCAUACGAGCU 1470
QY 462 CGCCAATGGCTCGGCCGAGTACAAGGTTCATCGGCTCGTGGACAGACCACTTCACCTCAG 521
Db 1471 GCGCAACGAUUCUGCCGAGUACAAGGUCAUUGGCUCCUGGACUGACCACTCAGCUUAG 1530
QY 522 AATAGACGAGTGCAGTGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT 581
Db 1531 AAUAGAGCGGAGUACUGCGCGGGAGCGGCGAGCAGCTGCGCGCGCGCGCGCGCGCG 1590
QY 582 GCCCTGCCAGCCCGGGAGCGAAGAACACTGTGAAGGCGCATGGCTGCTGTCGACATG 641
Db 1591 GCCCUGCCACCGGGUGAGCGGAAGACAGUAGAGGCGGCAUGCCUUGGUGGCGACUG 1650
QY 642 CGAGCCCTGCACCGGGTACCAAGTGGACCGCTACACCTGTAAAGACCTTGCCTTGA 701
Db 1651 CGAGCCUUGCACAGGGUACCAAGUAGGAGCGGCGUACACCTGUAAGAGCGUGUCCUA 1710
QY 702 CGACATGCGGCCACAGAGAACCGGACAGCTGCCAGCGCATCCCATCTGCTCAAGTTGA 761
Db 1711 UGACUAGCGGCCACAGAGAACCGGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1770
QY 762 GTGGAGCTCG 821
Db 1771 GUGGGCGCUCG 1830
QY 822 GCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
Db 1831 GUUGUUCUGGUGAUCACCUUUGGCGCUACAACGACAGCGCCCAUCGUCUAGGCGCG 1890
QY 882 CCGGGAACGTAGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941
Db 1891 CCGUGAACUGAGCUACGUGCUGGCGAGGCAUCUUCUGUGCUAUGCCACCCACCGUCC 1950
QY 942 CATGATCGCAGCGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1001
Db 1951 CAUGAUCGUCAGCG 2010
QY 1002 CATGAGCATCAGCTACG 1061
Db 2011 GAUGAGCAUGAUGAUGGCG 2070
QY 1062 CGAGGGCAACCGGTCGCTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1121
Db 2071 CGAGGGCAACCGGTCGCTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2130
QY 1122 CACCTTCATCTCATCTCCCTGCGAGCTGCTGCGGCACTGCGGTGCTGCTGCTGCTGCTG 1181
Db 2131 CACCTTCATCTCATCTCCCTGCGAGCTGCTGCGGCACTGCGGTGCTGCTGCTGCTGCTG 2190
QY 1182 CTCCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1241
Db 2191 CUCCACUUGGUGGUGGAGUUCUCCAGGACGAGGAGACUCCAGCCCGCGCGCGCGCGCG 2250
QY 1242 CGTCTCAAGTGCAGCATCTCGGACCTGCTCCTCTCATCTGCTGCTGCTGCTGCTGCTGCT 1301

[illegible]

RESULT 6

RESOUR		AAD38024	
ID	AAD38024	standard; DNA; 3431 BP.	
XX			
AC	AAD38024;		
DT	10-SEP-2002	(first entry)	
XX			
DE	Human metabotropic glutamate (mGluR4) receptor DNA.		
XX			
KW	Human; metabotropic glutamate receptor; mGluR4; neurodegeneration;		
KW	antipsychotic; anticonvulsant; analgesic; antidepressant; antiemetic;		
KW	gene; ds.		
XX			
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	26..2764	
FT		/*tag= a	
FT		/product= "Human metabotropic glutamate receptor"	
XX			
PN	US6384205-B1.		
XX			
PD	07-MAY-2002.		
XX			
PF	18-AUG-2000; 2000US-00641318.		
XX			
PR	12-MAR-1996; 96US-0013189P.		
PR	12-MAR-1997; 97US-00816178.		
XX			
PA	(ELIL) LILLY & CO ELI.		
XX			
PI	Belagaje RM, Wu S;		
XX			
DR	WFI; 2002-442818/47.		
DR	P-PSDB; AAE23757.		
XX			

RESULT 9
ADE07285/c
ID ADE07285 standard; DNA; 3884 BP.
XX AC
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QY 222 GGAGGGGAAGGTGCAGTTCCTGATTTGACGCTGTGTACGCCATGGGCCACGCGCTGCACGC 281
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DB 2449 CATGCACCGTACCTGTCTCCGGCCCGCTGCGGCTCTGCGCGCATGGACCCCGCTGGA 2390
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QY 402 TGTAACTTCAATGAGAACGAGACGACCGCGGCGCTACGACATCTACCAAGTACCAACT 461
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DB 2269 GCGCAACGATTTCTGCCGAGTACAGGTCATTTGGGCTCTGTGACATGACCACTGCACTT 2210
QY 522 AATAGCGGATGAGTGGCCAGGGAGTGGCCAGCAGCTGCGCGGCTCCATCTCGAGTCT 581
DB 2209 AATAGCGGATGAGTGGCCAGGGAGTGGCCAGCAGCTGCGCGGCTCCATCTCGAGTCT 2150
QY 582 GCCCTGCGAGCCCGGGAGCGAAAGAGACTGTGAAGGGCAATGGCTTGTGCTGGCACTG 641
DB 2149 GCCCTGCGAGCCCGGGAGCGAAAGAGACTGTGAAGGGCAATGGCTTGTGCTGGCACTG 2090
QY 642 CGAGCCCTGACCCGGGTACAGTACAGTACAGTGGAGCGCTACACCTGTGAAGACCTGCCCC 701
DB 2089 CGAGCCCTGACAGGGGTACAGTACAGTACAGTGGAGCGCTACACCTGTGAAGACCTGCCCC 2030
QY 702 CGACATCGGCCACACAGAACCGCACAGCTGCGAGCCATCCCATCGTCAAGTTGGA 761
DB 2029 TGACATCGGCCACACAGAACCGCACAGCTGCGAGCGCTGCGGCCATCCCATCATCAAGCTTGA 1970
QY 762 GTGGGACTCGCGCGGGCGCTGCTGCCCTCTTCTGCGCGCTGTGGGCAATCGCGCGCAC 821
DB 1969 GTGGGCTCGCGCTGCGCGCGCTGCTGCCCTCTTCTGCGCGCTGTGGGCAATCGCTGCCAC 1910
QY 822 GCTGTCGTGTGTACGTTTGTGCGCTACAGATACCCCATCGTCAAGGCTCGGG 881
DB 1909 GTTGTCTGTGTATCACTTTGTGCGCTAACAGCACGCGCATCGTCAAGGCTCGGG 1850
QY 882 CCGGGAATGAGTACGCTGCTGCGCGGCACTCTTCTGTGTACGCGCATCTCTTCT 941
DB 1849 CCGTGAATGAGTACGCTGCTGCGCGGCACTCTTCTGTGTATGCGCACCATCTTCT 1790
QY 942 CATGATCGAGAGCCGACCTGGGGACCTGTTGCTCGCGCGCATCTTCTTAGGGCTGG 1001
DB 1789 CATGATCGTGAAGCCGACCTTGGCACCTGCTGCGCGGCAATCTTCTTGGGACTAGG 1730
QY 1002 CATGAGCATGAGTACCGGGCCCTGTGACCAAGACCAACCGGATTTACCGCATCTTTGA 1061
DB 1729 GATGAGCATGAGTATGACGCGCTGCTCACCAAGACCAACCGCATCTACCGCATCTTGA 1670
QY 1062 GCAGGGCAAGGTCGCTGAGTGCCTGCGCTTTCATCAGCCCCGCGCTCGAGCTGGCCAT 1121
DB 1669 GCAGGGCAAGGTCGCTGAGTGCCTGCGCTTTCATCAGCCCCGCGCTCGAGCTGGCCAT 1610
QY 1122 CACCTTCATCTCATCTCCCTGACGCTGCTGCGCATCTGCGTGTGGTTCGTTGGTGGACCC 1181
DB 1609 CACCTTCAGCTCATCTGCTGACGCTGCTGGGCACTCTGTGTGGTTCGTTGGTGGACCC 1550
QY 1182 CTCCCATCTGCGTGTGACATTCAGGACCAACGAGACACTTGAACCCCGCTTTGCGAGGGG 1241
DB 1549 CTCCCATCTGCGTGTGACATTCAGGACCAACGAGACACTTGAACCCCGCTTTGCGAGGGG 1490
QY 1242 CGTCTCAAGTGCACATCTCGGACCTGCTCCCTCATCTGCTGCTGTGGCTACAGATGCT 1301
DB 1489 TGTGCTCAAGTGCACATCTCGGACCTGCTCCCTCATCTGCTGCTGTGGCTACAGATGCT 1430
QY 1302 GCTGATGCTCACGCTGCTACTGTGTACGCCATCAAGACCCGAGGGCTGCCCCGAGACCTTCAA 1361

Db 1429 GTCATGTCAGTCACCGTGTATGCCATCAAGACACCGCGTCCCGAGACCTTCAA 1370
 Qy 1362 CGAGGCCAAGCCCATCGGCTTCAACATGTACACCACTGCTGCTGTGCTGCGCTTCAAT 1421
 Db 1369 TGAGGCCAAGCCCATTTGGCTTCAACATGTACACCACTGCTGCTGTGCTGCGCTTCAAT 1310
 Qy 1422 CCCCATCTTTTGGACCTCAAGTCAGTCAGCCGACAGCTGTACATCCAGAACACACACT 1481
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 Qy 1482 GACGCTCTCGTGAGTCAGCGCTTCACTGTCCCTGGGGATGCTTACATGCCCAAGT 1541
 Db 1249 GACGCTCTCGTGAGTCAGCGCTTCACTGTCCCTGGGGATGCTTACATGCCCAAGT 1190
 Qy 1542 CTACATCATCTCTTCCACCGGAGCAGAACCTGTCCCAAGCGCAGCGAGCTTCAAAGC 1601
 Db 1189 CTACATCATCTCTTCCACCGGAGCAGAACCTGTCCCAAGCGCAGCGAGCTTCAAAGC 1130
 Qy 1602 CGTGTCACCGCGCCACCATGTCCAAAGTTTACACAGAGGGGCAACTTCAGGCCCAA 1661
 Db 1129 CGTGTCACCGCGCCACCATGTCCAAAGTTTACACAGAGGGGCAACTTCAGGCCCAA 1070
 Qy 1662 TCGGGAAGCCAAATCAGAGCTGTGTGAGAACCTTGGAGCCCGCAGCGCTGCCCAACCA 1721
 Db 1069 CGAGAGGCCAAAGTCTGAGCTCTGGAGAACCTTGGAGCCCGCAGCGCTGCCCAACCA 1010
 Qy 1722 GACCTACGTCACCTACCAACCATGCCCATCTAG 1755
 Db 1009 GACTACGTCACCTACCAACCATGCACTAG 976

RESULT 10

ID ACAS6476
 ACAS6476 standard; cDNA; 3884 BP.
 AC ACAS6476;
 XX
 DT 06-JUN-2003 (first entry)
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1074.
 XX
 KW Human; probe; ss; array element; Parkinson's disease;
 KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 XX
 OS Homo sapiens.

US6500938-B1.

31-DEC-2002.

30-JAN-1998; 98US-00016434.

30-JAN-1998; 98US-00016434.

(INCY-) INCYTE GENOMICS INC.

Au-Young J, Seilhamer JJ;

WPI; 2003-352189/33.

Combination of polynucleotide probes, useful as array elements in a microarray for monitoring the expression of a number of target polynucleotides.

Claim 1; SEQ ID NO 1074; 65pp; English.

The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the

CC diagnosis and treatment of cancer and immunopathology and neuropathology.
 CC The microarray is useful in diagnostics and treatment regimens, drug
 CC discovery and development, toxicological and carcinogenicity studies,
 CC forensics and pharmacogenomics. The microarray is also useful for
 CC monitoring progression of diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 CC and genomic fragments and in research and diagnostic applications. The
 CC array can detect changes in expression in a large number of genes coding
 CC for different signaling pathway populations which can be used to diagnose
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=06500938B1

XX Sequence 3884 BP; 734 A; 1265 C; 1080 G; 805 T; 0 U; 0 Other;

Query Match 83.8%; Score 1470.8; DB 10; Length 3884;
 Best Local Similarity 91.1%; Pred. No. 1.4e-307;
 Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

Qy 42 AGGGTTCCACCGATCTTCTCCAGCGCAGCTGACACACACACAGCGCGCAATCTGGTT 101
 Db 1196 AGGGTTCCACCGATCTTCTCCAGCGCAGCTGACACACACACAGCGCGCAATCTGGTT 1255
 Qy 102 TCCGAGTTCTGGGAGGACACTTCCATTGCAAGTTGAGCGCCACGCTCAAGAAGG 161
 Db 1256 TGCCGAGTTCTGGGAGGACACTTCCATTGCAAGTTGAGCGCCACGCTCAAGAAGG 1315
 Qy 162 AAGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGGCAGGACTCGGCCCTATGAGCA 221
 Db 1316 CAGCCACGTCAGAGTGCACCAACCGTGAGCGAATGGGCGAGGATTGAGCTTATGAGCA 1375
 Qy 222 GGAGGGGAAGTGCAGTTCTGTTGATGACGCTGTGTACGCCATGGGCGCAGCGCTGCACGC 281
 Db 1376 GGAGGGGAAGTGCAGTTCTGTTGATGACGCTGTGTACGCCATGGGCGCAGCGCTGCACGC 1435
 Qy 282 CATGCACCGTGACCTGTGTCGGCGCGGTAGGACTCTGCCCTCGCATGGACCCCGTGA 341
 Db 1436 CATGCACCGTGACCTGTGTCGGCGCGGTAGGACTCTGCCCTCGCATGGACCCCGTGA 1495
 Qy 342 TGGCACCACGCTGCTTAAGTATACATCAGGAACGTCAACTTCTCAGGCAATTCGCGGGAACCC 401
 Db 1496 TGGCACCACGCTGCTTAAGTATACATCAGGAACGTCAACTTCTCAGGCAATTCGCGGGAACCC 1555
 Qy 402 TGTAACTTCAATGAGAACCGAGACGACACCGGGCGCTACGACATCTACCACTACCACT 461
 Db 1556 TGTAACTTCAATGAGAACCGAGACGACACCGGGCGCTACGACATCTACCACTACCACT 1615
 Qy 462 GCGCAATGGCTCGGCGCGAGTACAGGTTCATCGGCTCGTGGACAGACACCTGCACCTCAG 521
 Db 1616 GCGCAATGGCTCGGCGCGAGTACAGGTTCATCGGCTCGTGGACAGACACCTGCACCTCAG 1675
 Qy 522 AATAGAGCGGATGCAAGTGGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT 581
 Db 1676 AATAGAGCGGATGCAAGTGGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT 1735
 Qy 582 CCCCTGCGAGCCCGGGAGCGAAAGAGATGTGAAGGGCATTGGCTTGTCTGGCAGCTG 641
 Db 1736 CCCCTGCGAGCCCGGGAGCGAAAGAGATGTGAAGGGCATTGGCTTGTCTGGCAGCTG 1795
 Qy 642 CGAGCCCTGCACCGGTTACCAAGTGCAGCGCTACACCTGTAGACCTGCCCTA 701
 Db 1796 CGAGCCCTGCACCGGTTACCAAGTGCAGCGCTACACCTGTAGACCTGCCCTA 1855
 Qy 702 CGACATGGGCGCCACAGAGAACCGCAGCAGCTGCCAGCGCCCATCCCATCTCAAGTTGA 761
 Db 1856 TGACATGGGCGCCACAGAGAACCGCAGCAGCTGCCAGCGCCCATCCCATCTCAAGTTGA 1915
 Qy 762 GTGGGACTCGCGGTGGGCGGTGCTGCTCTTCTCTGCGCGGTGGGCGATGCGCGCCAC 821

[illegible]

XX	22-APR-2004 (first entry)	Human polynucleotide probe #1074.	Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.	XX
OS	Homo sapiens.	US2004010136-A1.		XX
XX	15-JAN-2004.	26-NOV-2002; 2002US-00305720.		XX
FD		30-JAN-1998; 98US-00016434.		XX
PF	(INCY-) INCYTE GENOMICS INC.			XX
PR	Au-Young J, Seilhamer JJ;			XX
XX	WPI; 2004-090520/09.			XX
DR	New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic fragments.			XX
PT	Claim 6; SEQ ID NO 1074; 73pp; English.			XX
CC	The invention relates to a composition of polynucleotide probes comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes comprising at least a portion of a gene encoding a transducing polypeptide and third polynucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynucleotides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signalling pathway polypeptides. The composition can also be used to purify a subpopulation of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or ulcerative colitis, or a neuropathology, e.g. dementia, amnesia, epilepsy, Alzheimer's disease or depression. This sequence represents a human polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html .			XX
CC	Sequence 3884 BP; 734 A; 1265 C; 1080 G; 805 T; 0 U; 0 Other;			XX
CC	Query Match 83.8%; Score 1470.8; DB 12; Length 3884;			XX
CC	Best Local Similarity 91.1%; Pred. No. 1.4e-307;			XX
CC	Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;			XX
QY	42 AGGGTTCCGACCGGATCTCTCCAGCGCGACGCTGGACAAACAAAGGCGCAACATCTGGTT 101			XX
Db	1196 AGGCTTCGACCGCTACTCTTCAGCGCGACGCTGGACAAACAAAGGCGCAACATCTGGTT 1355			XX
QY	102 TGCCGAGTTCTGGGAGGACAACCTTCCATTCGAAGTTGAGCGCGCAACGCGCTCAAGAGGG 161			XX

Db 1256 TCCGAGTTCTGGGAGCAACTTCCACTGCAAGCTGAGCCGCCACGCCCTCAAGAGGG 1315
Qy 162 AAGCCACATCAAGAAAGTGACCAACCGAGAGCGCATCGGGCAGGACTCGGCCCTATGAGCA 221
Db 1316 CAGCCAGGTCAAGAAAGTGACCAACCGGTGAGCGAATTGGGCAAGGATTCAGCTTATGAGCA 1375
Qy 222 GAGGGGAAGTGCAAGTTGCTGATATGACGCTGTGTACGCCATGGGCCAGCGCTGACGC 281
Db 1376 GAGGGGAAGTGCAAGTTGCTGATCGATGCGGTGTACGCCATGGGCCAGCGCTGACGC 1435
Qy 282 CATGACCCGTGACCTGTGTCCCGGCGGTAGGACTCTGCCCTCGCATGACACCCCGTGA 341
Db 1436 CATGACCCGTGACCTGTGTCCCGGCGGTGGGCTCTGCCCGCATGACACCCCTGTGA 1495
Qy 342 TGGCACCCAGCTGTCTAAGTATACATCAGGAACGTCAACTTCTCAGGCAATTCGCGGAAACC 401
Db 1496 TGGCACCCAGCTGTCTAAGTATACATCGAAGACGTCAACTTCTCAGGCAATTCGCGGAAACC 1555
Qy 402 TGTAACTTCAATGAGAACCGAGAGACGACCGGGGCGCTAGACATCTACAGTACCAACT 461
Db 1556 TGTAACTTCAATGAGAACCGAGAGATGCGCTTGGGCGCTATGACATCTACCAATACCACT 1615
Qy 462 GGCCAATGCTCGGCGAGTACAAGTCAATCGCTCGTGGACAGACCACTTCACCTCAG 521
Db 1616 GGCCAATGCTCGGCGAGTACAAGTCAATCGCTCGTGGACAGACCACTTCACCTCAG 1675
Qy 522 AATAGACGGATGCAAGTGGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT 581
Db 1676 AATAGACGGATGCAAGTGGCCAGGAGCGGGCAGCAGCTGCGCGCTCCATCTGCAGCT 1735
Qy 582 GCCCTGCCAGCCCGGGAGCGAAAGAACTGTGAAGGCAATGGCTGTGCTGGACATG 641
Db 1736 GCCCTGCCAAACCGGGTGAGCGGAAGAGACAGTGAAGGCAATGGCTGTGCTGGACATG 1795
Qy 642 CGAGCCCTGCACCGGTAACAGTACCAAGTGAACCGCTACACCTGTAGACCTGCCCTTA 701
Db 1796 CGAGCCCTTGCAAGGGTACCAAGTACCAAGTGAACCGCTACACCTGTAGACCTGCCCTTA 1855
Qy 702 CGACATGGGGCCACAGAAACCGACGAGCTGCCAGCCCATCCCATCGTCAAGTTGA 761
Db 1856 TGACATGGGGCCACAGAAACCGACGAGCTGCCGGCCCATCCCATCATCAAGCTGA 1915
Qy 762 GTGGACATCGCGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 821
Db 1916 GTGGGCTCGCCCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1975
Qy 822 GCTGTTGCTGGTGCAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 881
Db 1976 GTTGTGCTGGTGCAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2035
Qy 882 CCGGAACTGAGCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941
Db 2036 CCGTGAACCTGAGCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2095
Qy 942 CATGATCGCAGAGCCGAGCTGGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1001
Db 2096 CATGATCGTGAAGCCGAGCTGGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2155
Qy 1002 CATGAGCATCAGTACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1061
Db 2156 GATGAGCATCAGTATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2215
Qy 1062 GCAGGGCAAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121
Db 2216 GCAGGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2275
Qy 1122 CACTTTCATCTCATCTCCCTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1181
Db 2276 CACTTTCAGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2335
Qy 1182 CTCACCATCGGTGGTGGACTTCCAGAACCAAGCAACCTTGAACCCCGCTTGGCAGGG 1241
Db 2336 CTCACCATCGGTGGTGGACTTCCAGAACCAAGCAACCTTGAACCCCGCTTGGCAGGG 2395

Qy 1242 CQTGCTCAAGTGCAGCATCTCGACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
Db 2396 TGTGCTCAAGTGTGACATCTCGGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2455
Qy 1302 CQTGATGCTCAGTGTACTGTGACGCTCAAGACCCGAGCGGTGCGGAGCCTTCAA 1361
Db 2456 GCTCATGTGCTCAGTGTGACGCTGATGCCATCAAGACACGCGGCTGCGGAGCCTTCAA 2515
Qy 1362 CGAGCCCAAGCCCATCGGCTTCCACCATGTACACCACTGTGCTGCTGCTGCTGCTGCTGCT 1421
Db 2516 TGAGGCCAAGCCCATTTGGCTTCCACATGTACACCACTGTGCTGCTGCTGCTGCTGCT 2575
Qy 1422 CCCCATCTTTTGTGCACTCAGTCAAGCGGACCAAGTGTATCATCCAGAACCACT 1481
Db 2576 CCCCATCTTTTGGCACTCCTGCACTCGGCGGCAAGCTGTATCATCCAGACGAGCT 2635
Qy 1482 GACGCTCTCGTGTGCTGAGCGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
Db 2636 GACGCTCTCGGCTGAGTCTGAGCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2695
Qy 1542 CTACATCATCTCTTCCACCCGAGCAGAACGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1601
Db 2696 CTACATCATCTCTTCCACCCGAGCAGAACGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2755
Qy 1602 CQTGCTACCCGCGCCCATGTCCAAAGTTCAACAGAGGCAACTTCAGGCCCCAA 1661
Db 2756 CQTGCTTACGGCGGCGCCCATGTCCAAAGTTCAACAGAGGCAACTTCAGGCCCCAA 2815
Qy 1662 TGGGAAAGCCAAATCAGAGCTGTGTGAGAACTTGAGAGCCCGGCTGCTGCTGCTGCTGCT 1721
Db 2816 CGGAGAGCCAAAGTGTGAGCTCTGCGAAGACCTTGAGGCCCCCAGGCTGCTGCTGCTGCTGCT 2875
Qy 1722 GACCTACCTGCTACACCAACCATGCCATCTAG 1755
Db 2876 GACTTACCTGCTACACCAACCATGCCATCTAG 2909

RESULT 12

ADQ89113

ID ADQ89113 standard; cDNA; 3884 BP.

XX AC ADQ89113;

XX DT 21-OCT-2004 (first entry)

XX DE Human urological disorder related protein 115 encoding cDNA SEQ.65.

XX KW urological disorder; uropathic; cytostatic; urinary incontinence;

XX KW benign prostatic hyperplasia; human; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 171..2909

XX FT /*tag= a

XX FT /product= "urological disorder related protein 115"

XX XX WO2004065576-A2.

XX XX 05-AUG-2004.

XX XX 14-JAN-2004; 2004WO-US000750.

XX XX 15-JAN-2003; 2003US-0440318P.

XX XX 04-FEB-2003; 2003US-044783P.

XX XX 27-MAR-2003; 2003US-0457901P.

XX XX 08-MAY-2003; 2003US-0468775P.

XX XX 19-JUN-2003; 2003US-0471614P.

XX XX 16-JUL-2003; 2003US-0478742P.

XX XX 18-JUL-2003; 2003US-0488529P.

XX XX 30-JUL-2003; 2003US-0491156P.

XX XX 02-SEP-2003; 2003US-0499594P.

PR	26-SEP-2003; 2003US-0506332P.
XX	(MILL-) MILLENNIUM PHARM INC.
PA	Karicheti V, Silos-Santiago I, Eliasof SD;
XX	WPI; 2004-562167/54.
PI	P-PSDB; ADQ89114.
XX	
DR	Use of polypeptides related to urological disorders, e.g. 44390, 54181,
XX	PT 211 or for identifying a compound capable of treating a urological
XX	PT disorder or identifying and treating a subject having a urological
XX	PT disorder.
XX	
XX	Claim 1; SEQ ID NO 65; 542pp; English.
XX	
CC	The present invention describes the use of polypeptides related to
CC	urological disorders for identifying a compound capable of treating a
CC	urological disorder, identifying a subject having a urological disorder,
CC	or treating a subject having a urological disorder. Also described: (1) a
CC	method for identifying a compound capable of treating a urological
CC	disorder; (2) a method for identifying a subject having a urological
CC	disorder; and (3) a method for treating a subject having a urological
CC	disorder. The compound has utrophathic and cyostatic activities. The
CC	polypeptides related to urological disorders are useful for identifying a
CC	compound capable of treating a urological disorder, identifying a subject
CC	having a urological disorder, or treating a subject having a urological
CC	disorder. Disorders include urinary incontinence and benign prostatic
CC	hyperplasia. The present sequence encodes a human urological disorder
CC	related protein, which is used in the exemplification of the present
CC	invention.
XX	
QQ	Sequence 3884 BP; 734 A; 1265 C; 1080 G; 805 T; 0 U; 0 Other;
QQ	
Query Match	83.8%; Score 1470.8; DB 13; Length 3884;
Best Local Similarity	91.1%; Pred. No. 1.4e-307;
Matches 1562; Conservative	0; Mismatches 152; Indels 0; Gaps 0;
QY	42 AGGTTTCGACCGATACTTCTCCAGCCGCACGCTGGACAACAAAGGCGCAACATCTGGTT 101
DB	
	1196 AGGTTTCGACCGCTACTTCTCCAGCCGCACGCTGGACAACAAAGGCGCAACATCTGGTT 1255
QY	102 TGCCGAGTTCTGGGAGGACAACATTCATATGCCAGTTTGAGCCGCCACCGCTCAAGAAGGG 161
DB	
	1256 TGCCGAGTTCTGGGAGGACAACATTCCTACTGCAAGCTGAGCGGCCACGCCCTCAAGAAGGG 1315
QY	162 AGCCCATCAAGAGTGCACCAACCAGAGCGGATCGGGCAGGACTCGGCGCTATGACGA 221
DB	
	1316 CAGCCAGTCAAGAAGTGCACCAACCCTGAGCGAATTTCGGGCAGGATTCAGCTTATGACGA 1375
QY	222 GGAGGGGAAGGTGCAGTTCTGTGATTGACGTGTGTAGCCATGGGCCACCGCTGCACGC 281
DB	
	1376 GGAGGGGAAGGTGCAGTTCTGTGATTGACGTGTGTAGCCATGGGCCACCGCTGCACGC 1435
QY	282 CATGCACCGTGACCTGTGTCCCGCCCGGTAGGACTCTGCCCCTCGCATGGACCCCCGTGGA 341
DB	
	1436 CATGCACCGTGACCTGTGTCCCGCCCGGTGGGCTCTGCCCGGCGCATGGAOCCTGTAGA 1495
QY	342 TGGCACCCAGCTGCTTAAGTACATPCAGGAAGCTCAAATTTCTAGGCATATGCGGGGAACCC 401
DB	
	1496 TGGCACCCAGCTGCTTAAAGTACATPCGAAACGTCAACTTCTCAGGCATCGCAGGAACCC 1555
QY	402 TGTAACTTCAATGAGAACGGNAGCGCACCGGGGGCTACGACATCTTACAGTACCRACT 461
DB	
	1556 TGTGACCTTCAATGAGAAATGGAGATGGCGCTTGGCGGCTATGACATCTACCAATACCACT 1615
QY	462 GCGCAATGGGCTCGGCCGAGTACAGGTCATCGGCTCGTGGACAGACCAACCTGCACCTCAG 521
DB	
	1616 GCGCAACGATTTCTCCGAGTACAAGTCAATTTGGTCTCTGGACTGACCACTGCACCTTAG 1675
QY	522 AATAAGCGGATGCAATGGCCAGGGAGTGGCCAGCAGCTGCCGCGTCCAATCTGCAGTCT 581
DB	
	1676 AATAGCGGATGCACTGGCCGGGAGCGGGCAGCAGCTGCCCGCTCCAATCTGCAGCTCT 1735

QY 1662 TGGGGAAGCCAAATCAGAGCTGTGTGAGAACCTGGAGAGCCCGAGCGCTGCTACCAACA 1721
Db 2816 CGGAGAGGCCAAGTCTGAGCTCTGCGAGAACCTTGAGGGCCCGAGCGCTGGCCACCAACA 2875
QY 1722 GACCTACGTCACTACACCAACCATGCCATCTAG 1755
Db 2876 GACTTACGTCACTTACACCAACCATGCCATCTAG 2909

RESULT 13

AAT03888

ID AAT03888 standard; DNA; 3880 BP.

XX AAT03888;

XX 22-DEC-1995 (first entry)

XX Human mGluR4 gene.

XX Metabotropic glutamate receptor 4; mGluR4; stroke; epilepsy;
KW Alzheimer disease; detection; diagnosis; therapy; ds.
XX Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 171..2909

FT /*tag= a

XX

PN W09522609-A2.

XX

XX 24-AUG-1995.

XX

XX 21-FEB-1995; 95WO-GB000356.

XX

XX 21-FEB-1994; 94GB-00003285.

XX

XX 01-AUG-1994; 94GB-00015532.

XX

XX (WELL) WELLCOME FOUND LTD.

XX

XX Makoff AJ;

XX

XX WPI; 1995-302715/39.

XX

XX P-PSDB; AAR82658.

XX

PS New isolated human metabotropic glutamate receptors - used for detection,
PT diagnosis and therapy of diseases associated with the receptors, eg.
PT stroke, epilepsy and Alzheimer's disease.

XX Claim 4; Page 35-40; 55pp; English.

XX mRNA from the human cerebellum was used to construct a cDNA library. cDNA
CC was amplified by PCR primers (AAT03888-97) based on rat mGluR4 sequences
CC and with the primers given in AAT03888-99 to obtain cDNA encoding human
CC mGluR4

XX Sequence 3880 BP; 734 A; 1264 C; 1080 G; 802 T; 0 U; 0 Other;

Query Match 83.7%; Score 1469.2; DB 2; Length 3880;
Best Local Similarity 91.1%; Pred. No. 3e-307;

Matches 1561; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 42 AGGGTTTCGACCGATCTTCTCCAGCGCGACGCTGGACAAACAGCGCGCAACATCTGGTT 101

Db 1193 AGGTTTCGACCGCTACTTCTCCAGCGCGACGCTGGACAAACAGCGCGCAACATCTGGTT 1252

QY 102 TGGCGAGTTCTGGAGGACAACTTCCATTGCAAGTTGACCGCGCAGCGCTCAAGAAGGG 161

Db 1253 TGGCGAGTTCTGGAGGACAACTTCCATTGCAAGTTGACCGCGCAGCGCTCAAGAAGGG 1312

QY 162 AAGCCACATCAAGAGTGACCAACCGAGAGCGCATCGGCGAGGACTCGGCGCTATGAGCA 221

Db 1313 CAGCCACGTCAAGAGTGACCAACCGAGAGCGCATCGGCGAGGATTTCAGCTTATGAGCA 1372

QY 222 GGAGGGGAAGGTGCAGTTGTCGTGATTTGACGCTGTGTATAGCGCATGGGCGACGCGCTGCACGC 281
Db 1373 GGAGGGGAAGGTGCAGTTGTCGTGATTTGTCGATCGATGTCGCGTGTATAGCGCATGGGCGACGCGCTGCACGC 1432
QY 282 CATGACACCGTGACCTGTGTCCCGGCGCGGTAGGACTCTGCGCCCTCGCATGGACCCCGTGA 341
Db 1433 CATGACACCGTGACCTGTGTCCCGGCGCGGTGCGGCTCTGCGCGCGCATGGACCCCGTGA 1492
QY 342 TGGCACCCAGCTGCTTAAAGTACATCAGGAAAGTCAACTTCTCAGGCAATTCGCGGGAACCC 401
Db 1493 TGGCACCCAGCTGCTTAAAGTACATCAGGAAAGTCAACTTCTCAGGCAATTCGCGGGAACCC 1552
QY 402 TGTAACTTCAATGAGAACGGAGACGACCGGGGGCGCTACGACATCTACCACTACCACT 461
Db 1553 TGTAACTTCAATGAGAACGGAGATGCGCTGCGGCGCTATGACATCTACCACTACCACT 1612
QY 462 GCGCAATGCTCGGCGGAGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGT 521
Db 1613 GCGCAATGCTCGGCGGAGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGT 1672
QY 522 AATAGAGCGGATGCAAGTGGCCAGGAGTGGCCAGAGCTGGCCGCGCTCCATCTGCAGTCT 581
Db 1673 AATAGAGCGGATGCAAGTGGCCAGGAGTGGCCAGAGCTGGCCGCGCTCCATCTGCAGTCT 1732
QY 582 GCCCTGCCAGCCCGGGAGCGGAAAGAAAGTGTGAAGGCAATGGCTTGTGCTGCGCACTG 641
Db 1733 GCCCTGCCAGCCCGGGAGCGGAAAGAAAGTGTGAAGGCAATGGCTTGTGCTGCGCACTG 1792
QY 642 CGAGCCCTGCAACCGGCTACAGTACCAAGTGGACCGCTACAGCTGTGAAGACCTGCCCTTA 701
Db 1793 CGAGCCCTGCAACCGGCTACAGTACCAAGTGGACCGCTACAGCTGTGAAGACCTGCCCTTA 1852
QY 702 CGACATGGGCGCCACAGAGAACCGCACGAGCTGCCAGCGCATCCCGCATCGTCAAGTTGA 761
Db 1853 TGACATGGGCGCCACAGAGAACCGCACGAGCTGCCAGCGCATCCCGCATCGTCAAGTTGA 1912
QY 762 GTGGACCTCGCGGTGGCGGTGCTGCCCTCTTCTTCTGCGCGGTGGGATCGCGCGCAC 821
Db 1913 GTGGGCTCGCGGTGGCGGTGCTGCCCTCTTCTTCTGCGCGGTGGGATCGCGCGCAC 1972
QY 822 GCTGTTGCTGGTGTGACGTTGTCGCTACAAAGTGGACCGCTACAGCTGTGAAGACCTGCCG 881
Db 1973 GTGTTGCTGGTGTGACGTTGTCGCTACAAAGTGGACCGCTACAGCTGTGAAGACCTGCCG 2032
QY 882 CGGGAACTGAGCTACGTGCTGCTGGCGGCGATCTTCTGTGCTACGCGCATCTACCTTCT 941
Db 2033 CGGTGAATGAGCTACGTGCTGCTGGCAGGATCTTCTGTGCTATGCCACCATCTTCT 2092
QY 942 CATGATCGAGAGCGGACCTGCGGACCTGTTGCTGCGCGCGATCTTCTAGGGCTCGG 1001
Db 2093 CATGATCGAGAGCGGACCTTGGCACCTGCTGCTGCGCGCGAATCTTCTGCGGACTAGG 2152
QY 1002 CATGAGCATGACTAGCGGCGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGA 1061
Db 2153 GATGAGCATGACTATGAGCGCTGCTCACCAGACCAACCGCATCTACCGCATCTTGA 2212
QY 1062 CGAGGCGAAACGCTCGGTGAGTGGCGCTGTTTATCAGCGCGGCTCGAGCTGGCCAT 1121
Db 2213 CGAGGCGAAACGCTCGGTGAGTGGCGCTGTTTATCAGCGCGGCTCGAGCTGGCCAT 2272
QY 1122 CACTTTCATCTCATCTCCCTGAGCTGCTCGGCAATCTGCGGTGCTGGTTCGTGGTGAACCC 1181
Db 2273 CACTTTCATCTCATCTCCCTGAGCTGCTCGGCAATCTGCGGTGCTGGTTCGTGGTGAACCC 2332
QY 1182 CTCCCACTCGGTGGTGGACTTCCAGGACCAACCGGACATTTGACCCCGCTTGGCCAGGG 1241
Db 2333 CTCCCACTCGGTGGTGGACTTCCAGGACCAACCGGACATTTGACCCCGCTTGGCCAGGG 2392
QY 1242 CGTGTCAAGTGCACATCTCGGACCTGTCCCTCATCTGCGCTGTGGGTACAGCATGCT 1301
Db 2393 TGTGTCAAGTGTGACATCTCGGACCTGTCCCTCATCTGCGCTGTGGGTACAGCATGCT 2452
QY 1302 GCTGATGCTGACGTGTACTGTGTACGCCATCAAGACCCGAGGCGGTGCCGAGACCTTCAA 1361

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Qy 942 CATGATCGAGAGCCGAGACCTGGGACCTGTTCGTCCGCGCATCTTCTAGGGCTCG 1001
Db 1926 CATGATCGCTGAGCCGACCTTGGCACCTGCTGCTGCGCGAATCTTCTGGAGTAG 1985
Qy 1002 CATGACATCAGTACGCGGCTGCTGACCAAGACCAACCGCATTTACGGCATCTTGA 1061
Db 1986 GATGACATCAGTATGACGCTGCTGACCAAGACCAACCGCATTTACGGCATCTTGA 2045
Qy 1062 GCAGGGCAACGCTGCTGAGTCCGCGCTTTCATCAGCCGCGCTGCGAGCTGCCAT 1121
Db 2046 GCAGGGCAAGGCTGCTGAGTCCGCGCTTTCATCAGCCGCGCTGCGAGCTGCCAT 2105
Qy 1122 CACCTTCATCTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181
Db 2106 CACCTTCAGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2165
Qy 1182 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
Db 2166 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2225
Qy 1242 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
Db 2226 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2285
Qy 1302 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1361
Db 2286 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2345
Qy 1362 CGAGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421
Db 2346 TGAGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2405
Qy 1422 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1481
Db 2406 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2465
Qy 1482 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
Db 2466 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2525
Qy 1542 CTATCATCTCTCTTCCACCGGAGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1601
Db 2526 CTATCATCTCTCTTCCACCGGAGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2585
Qy 1602 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1661
Db 2586 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2645
Qy 1662 TGGGGAAGCAATCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1721
Db 2646 CCGAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2705
Qy 1722 GACCTACGTCACCTACCAACCAATGCCATCTA 1754
Db 2706 GACTTACGTCACCTACCAACCAATGCCATCTA 2738

RESULT 15
ADRO6667
ID ADRO6667 standard; cDNA; 3470 BP.
XX
AC ADRO6667;
XX
DT 04-NOV-2004 (first entry)
XX
DE Full length human cDNA useful for treating neurological disease Seq 173.
XX
KW gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;

KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW tranquiliser.
XX
OS Homo sapiens.
XX
PN EP1447413-A2.
XX
PD 18-AUG-2004.
XX
PF 12-FEB-2004; 2004EP-00003145.
XX
PR 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI Wakamatsu A, Ishii S, Nagai K, Irie R,
XX
DR WPI; 2004-583265/57.
DR P-PSDB; ADR06623.
XX
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 173; 2686pp; English.
XX
CC This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunoassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC cytostatic and tranquiliser activities. This polynucleotide is a full
CC length human cDNA sequence of the invention. NOTE: This sequence is not
CC given in the sequence listing of the specification but can be obtained on
CC CD-ROM from the European Patent Office, Vienna Sub-office.
XX
SQ Sequence 3470 BP; 677 A; 1098 C; 935 G; 760 T; 0 U; 0 Other;

Query Match 81.1%; Score 1422.8; DB 13; Length 3470;
Best Local Similarity 90.9%; Pred. No. 3.1e-297;
Matches 1514; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
Qy 42 AGGGTTCCACCGATATCTTCAGCCGCGACCTGACCAACACAGCGCGCAACATCTGGTT 101
Db 580 AGGCTTCAGCCGCTACTTCTCAGCCGCGACCTGACCAACACCGCGCGCAACATCTGGTT 639
Qy 102 TGCCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCCGCGCGCTCAAGAGGG 161
Db 640 TGCCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCCGCGCGCTCAAGAGGG 699
Qy 162 AAGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGGCAGAGTCTGGCTTATGAGCA 221
Db 700 CAGCCACGTCAGAGTGCACCAACCGTGCAGCAGTTCGGCAGGATTCAGCTTATGAGCA 759
Qy 222 GGAGGGGAAGTGCAGTTCGTGATGAGCTGTGTACGCCATGGGCCAGCGCTCAGCG 281
Db 760 GGAGGGGAAGTGCAGTTCGTGATGAGCTGTGTACGCCATGGGCCAGCGCTCAGCG 819
Qy 282 CATGCACCGTGCACCTGTGCTCCGCGCGGTGAGGACTCTGCCCTGCATCGACCCGTTGA 341
Db 820 CATGCACCGTGCACCTGTGCTCCGCGCGGTGAGGACTCTGCCCTGCATCGACCCGTTGA 879
Qy 342 TGGCACCCAGCTGCTTAAGTATACAGGAACGTCAACTTCTCAGGCAATTGCGGGGAACCC 401

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Db 880 TGGCACCAGCTGCTTAAGTACATCCGAAACGTCAACTTCTCAGSCATCGCAGGGAACCC 939
Qy 402 TGTAACTTCAATGAGAACGAGACGCAACCGGGGCGCTACGACATCTTACCAAGTACCAACT 461
Db 940 TGTGACCTTCAATGAGAAATGAGATGCGCTCGGGCGCTATGACATCTTACCAATACCAAGCT 999
Qy 462 GCGCAATGGCTCGGCGGAGTACAAGGTCAATCGGCTCGTGGACAGACACCACTGCAACCTCAG 521
Db 1000 GCGCAACGATTTGCGCGAGTACAAGGTCAATGGCTTCCTGGACTGACCACTGCAACCTTAG 1059
Qy 522 AATAGACGGATGCAAGTGGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAAGTCT 581
Db 1060 AATAGACGGATGCACTGGCCGGGAGCGGGCAGCAGCTGCGCGCTCCATCTGCAAGCT 1119
Qy 582 GGCCTGCAAGCCCGGGAGCGGAAGACATGTGTGAAGGGCATGGCTTGTGCTGTGGCACTG 641
Db 1120 GGCCTGCAAGCCCGGGAGCGGAAGACATGTGAAGGGCATGGCTTGTGCTGTGGCACTG 1179
Qy 642 CGAGCCCTGCAACCGGGTACCAAGTACCAAGTGGACCGCTACACCTGTAGACCTGCCCTTA 701
Db 1180 CGAGCCCTTGCACAGGGTACCAAGTACCAAGTGGACCGCTACACCTGTAGACCTGTCCCTA 1239
Qy 702 CGACATGGGGCCACAGAGAACCGCAACGAGTGGCCAGGCCCATCCCATCGTCAAGTTGGA 761
Db 1240 TGACATGGGGCCACAGAGAACCGCAACGAGTGGCCAGGCCCATCCCATCATCAAGTTGA 1299
Qy 762 GTGGACATCGCGTGGGCGGTGCTGCCCTCTTCTTGGCGGTGGTGGGCACTGCGGCCAC 821
Db 1300 GTGGGCTCGCGTGGGCGGTGCTGCCCTCTTCTTGGCGGTGGTGGGCACTGCTGCCAC 1359
Qy 822 GCTGTTGCTGGTGGTCAAGTGTGGCGCTACAAGTACACCGCATCCCGCATCGTCAGGCGCTCGG 881
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Search completed: June 21, 2005, 05:02:17
Job time : 999 secs

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 01:57:35 ; Search time 7720 Seconds
(without alignments)
11015.402 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 1755

Sequence: 1 atgccagggtatcatc.....acaccacacatgccatctag 1755

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1712.4	97.6	4488	10	RATMGLUR4A
2	1707.6	97.3	2838	6	AR381454 Sequence
3	1707.6	97.3	3704	10	RATMGLURBD
4	1560.4	88.9	4425	10	BC072635 Mus muscu
5	1516.4	86.4	3868	10	RNU47331
6	1470.8	83.8	3176	9	AK122982
7	1470.8	83.8	3431	6	AR208972
8	1470.8	83.8	3431	9	HSU92457
9	1470.8	83.8	3431	9	HSU92457
10	1470.8	83.8	3850	9	AK122836
11	1470.8	83.8	3884	6	A61196
12	1470.8	83.8	3884	6	AR270511
13	1470.8	83.8	3884	6	AR381464
14	1470.8	83.8	3884	6	AX548890 Sequence
15	1470.8	83.8	3884	6	AX548890 Sequence
16	1470.8	83.8	3884	6	AX548890 Sequence
17	1469.8	83.7	2738	6	AX3637
18	1469.8	83.7	2738	6	AX427263
19	1467.8	83.6	2736	6	AR149574

20	1422.8	81.1	3470	6	CQ849704	CQ849704 Sequence
21	1422.8	81.1	3470	9	AK126746	AK126746 Homo sapi
22	1340.6	76.4	3590	6	CQ853450	CQ853450 Sequence
23	1340.6	76.4	3590	9	AK131536	AK131536 Homo sapi
24	1331.2	75.9	2548	6	CQ730036	CQ730036 Sequence
25	1281.4	73.0	3002	10	BC080284	BC080284 Mus muscu
26	935.8	53.3	221062	2	AC134369	AC134369 Rattus no
27	916	52.2	2041	5	AB042755	AB042755 taenlopyg
28	880.6	50.2	2961	6	AR071655	AR071655 Sequence
29	880.6	50.2	2961	6	AR202435	AR202435 Sequence
30	880.6	50.2	6122	6	AX548894	AX548894 Sequence
31	871	49.6	2670	6	AR106168	AR106168 Sequence
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33	859.8	49.0	2727	10	AY673682	AY673682 Mus muscu
34	855	48.7	2793	10	RNU63288	U63288 Rattus norv
35	851.8	48.5	2830	6	AX418281	AX418281 Sequence
36	851.8	48.5	2830	10	MMU17252	U17252 Mus musculu
37	849	48.4	213609	10	AC127341	AC127341 Mus muscu
38	843.8	48.1	3212	4	AY275542	AY275542 Oryctolag
39	842.2	48.0	2727	9	HSU95025	U95025 Homo sapien
40	839	47.8	3321	6	AR147650	AR147650 Sequence
41	839	47.8	3321	6	AR147651	AR147651 Sequence
42	839	47.8	3321	6	AX548898	AX548898 Sequence
43	839	47.8	3321	6	AX658362	AX658362 Sequence
44	839	47.8	3321	9	HSU92459	U92459 Human metab
45	833.2	47.5	4418	10	RATMGLUR6	DI3963 Rattus norv

ALIGNMENTS

RESULT 1								
RATMGLUR4A								
LOCUS	RATMGLUR4A	4488 bp	mRNA	linear	ROD 01-APR-1996			
DEFINITION	Rat metabotropic glutamate receptor (GLUR4) mRNA, complete cds.							
ACCESSION	M90518							
VERSION	M90518.1	GI:205400						
KEYWORDS	metabotropic glutamate receptor.							
SOURCE	Rattus norvegicus (Norway rat)							
ORGANISM	Rattus norvegicus							
REFERENCE	1 (bases 1 to 4488)							
AUTHORS	O'Hara,P.J., Sheppard,P.O., Thogersen,H., Venezia,D., Haldeman,B.A., McGrane,V., Houamed,K.M., Thomsen,C., Gilbert,T.L. and Mulvihill,E.R.							
TITLE	The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins							
JOURNAL	Neuron 11 (1), 41-52 (1993)							
MEDLINE	93332699							
PUBMED	8338667							
REFERENCE	2 (bases 1 to 4488)							
AUTHORS	O'Hara,P.J.							
TITLE	Direct Submission							
JOURNAL	Submitted (01-APR-1992) Patrick J. O'Hara, ZymoGenetics, Inc., Seattle, WA 98105, USA							
COMMENT	Original source text: Rattus norvegicus cDNA to mRNA.							
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	/tissue_type="brain"							
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	/note="putative"							
	/codon_start=1							
	/product="metabotropic glutamate receptor"							

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Qy	1242	CGTGCTCAAGTGCACATCTCGGACCTGCTCCTCATCTGCTGCTGGGCTACAGCATGCT	1301
Ds	2971	TGTGCTCAAGTGTGACATCTCGGACCTGCTCCTCATCTGCTGCTGGGCTACAGCATGCT	3030
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Ds	3031	GCTGATGTGACGTGTACTGTGTAGCCATCAAGACCGAGCGGTGCCGAGACTTCAA	3090
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Ds	3091	TGAGGCCAAGCCCATCGGCTTACCATGTACACACCTGCAATGTCTGGCTGGCTTCAT	3150
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Ds	3151	CCCCATCTTTTGGCACTTCCAGCTACGCGACCAAGCTGTATCATCCAGACCAACACACT	3210
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Ds	3211	GACGCTCTCTGAGTCTGAGCGCTTCAAGTGTCTGCTGCTGGGATGCTCTACATGCCCAAGT	3270
Qy	1542	CTACATCATCTCTTCCACCGGAGCAGACGTGCGCCCAAGCGCAAGCGCAGTCTCAAGC	1601
Ds	3271	CTACATCATCTCTTCCACCGGAGCAGACGTGCGCCCAAGCGCAAGCGCAGTCTCAAGC	3330
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Ds	3331	CGTTGTACCCGCGCACCATGTCCCAAGTTCACACAGAGGCGCACTTCAGGCCCAA	3390
Qy	1662	TGGGAAAGCCAAATCAGAGCTGTGTGAGAACTGTGAGACCCCGCTGGCTTACAAACA	1721
Ds	3391	TGGGAAAGCCAAATCAGAGCTGTGTGAGAACTGTGAGACCCCGCTGGCTTACAAACA	3450
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RESULT 5			
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LOCUS	RNU47331	3868 bp	mRNA
DEFINITION	Rattus norvegicus metabotropic glutamate receptor 4b mRNA, complete cds.		
ACCESSION	U47331		
VERSION	U47331.1	GI:1197725	
KEYWORDS	Rattus norvegicus (Norway rat)		
SOURCE	Rattus norvegicus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		
REFERENCE	1 (bases 1 to 3868)		
AUTHORS	O'Hara, P.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-JAN-1996) Patrick J. O'Hara, ZymoGenetics, 1201 Eastlake Avenue East, Seattle, WA 98102, USA		
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ORIGIN

Query Match	86.4%	Score 1516.4	DB 10	Length 3868
Best Local Similarity	99.9%	Pred. No. 5.6e-241		
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Qy	102	TGCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCGCGCCACCGCTCAAGAGGG	161	
Ds	1940	TGCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCGCGCCACCGCTCAAGAGGG	1999	
Qy	162	AAGCCACATCAAGAAAGTGCCACCAACCGAGAGCGCATCGGCGAGGACTCGGCTATGAGCA	221	
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Qy	222	GGAGGGAAAGTGCGATTGATGACGCTGTGTACGCCATGGGCCACCGCGCTGCACGC	281	
Ds	2060	GGAGGGAAAGTGCGATTGATGACGCTGTGTACGCCATGGGCCACCGCGCTGCACGC	2119	
Qy	282	CATGCAACCGTACCTGTCCTCGGCGCGCTAGGACTCTGCCCTCGCATGGACCCCGTGA	341	
Ds	2120	CATGCAACCGTACCTGTCCTCGGCGCGCTAGGACTCTGCCCTCGCATGGACCCCGTGA	2179	
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Ds	2480	CGAGCCCTGCACCGGTTACCAAGTACCGGCTGAGCGGCTTACACCTGTAGACCTGCCCTTA	2539	
Qy	702	CGACATGCGGCCACAGAGAACCGCAGAGCTGCCAGCCCATCCCCATCGTCAAGTTGGA	761	
Ds	2540	CGACATGCGGCCACAGAGAACCGCAGAGCTGCCAGCCCATCCCCATCGTCAAGTTGGA	2599	
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880	Db	TGCCGAGTTCTTGGGAGGACAACTTCCATGCAAGCTGAGCGGCCACGCGCTCTAAGAAAGG	939
162	Qy	AAGCCACATCAAGAAGTGCAACAAACGAGAGCGCATCGGGCAGAGACTCGCGCTATGAGCA	221
940	Db	CAGCCACGTCDAAGAAGTGCAACCAACCGTGAGCGAATTGGGCAGGATTCAGCTTATGAGCA	999
222	Qy	GGAGGGAAAGGTGCAGTTTCGTGATTGACGTGTGTATACGCCATNGGGCCACGCGCTGCAAGC	281
1000	Db	GGAGGGAAAGGTGCAGTTTGTGATCGATCGCGTGTACGCCATNGGGCCACGCGCTGCACGC	1059
282	Qy	CATGCACGCTGACCTGTGTCCCGCGCGGTAGGACTTGCCTCGCATNGGACCCCGTGGGA	341
1060	Db	CATGCACGCTGACCTGTGTCCCGCGCGGTGGGCTCTGCGCGGCATNGGACCCCTGTAGA	1119
342	Qy	TGGCACCCAGCTGTCTTAAGTACATCAGAAAGCTCAAATTCTCAGGCATTTGCGGGAAACCC	401
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402	Qy	TGTAACCTTCAATGAGAAACGAGACGCAACCGGGCGCTACGACATCTACAGTACCAACT	461
1180	Db	TGTGACCTTCAATGAGAAATGGAGATGCGCTCGGGCGCTATGCATCTACCAATACCAAGCT	1239
462	Qy	GCGCAATGGCTCGGCGGAGTACAGGTATCGGCTCGTGGACAGACACACCTGCACCTCAG	521
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522	Qy	AATAGAGCGGATGCACTGGCCAGGGAGTGGCCAGCAGCTGCGCGGCTCCATCTGCACTCT	581
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1480	Db	TGACATGGGGCCACAGAGAACCGCAGGGCTGCGGGCCCATCCCATCATCAAGCTTGA	1539
762	Qy	GTGGGACTCGCCGTGGGCGGTGCTGCCCTCTTCTGTGGCGTGGTGGGSCATTCGCGCCAC	821
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1780	Db	GATGAGCATCAGCTATGAGCGCTTGTCAACCAAGACCAACCGCATCTACCGCATCTTCGA	1839
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Qy	1542	CTACATCATCTCTTCCACCCGGAGCAGAACTGTCCTCAAGCGCAAGCGCAAGTCTCAAAGC	1601
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LOCUS	AR208972	3431 bp	linear
DEFINITION	Sequence 1 from patent US 6384205.		
ACCESSION	AR208972		
VERSION	AR208972.1	GI:21510266	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 3431)		
AUTHORS	Belagaje,R.M. and Wu,S.		
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Best Local Similarity	91.1%;	Pred. No. 2e-233;	
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Qy	102	TGCCGAGTTCTGGGAGGACCAATCTTCAATTGCAAGTTGAGCGCCACGCGCTCAAGAAAGG	161
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Qy	162	AAGCCACATCAGAAAGTGTGACCAACCGAGAGCGCATCGGGAGGATCTGGGCTATGAGCA	221
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RESULT 9
HSU92457 3431 bp mRNA linear PRI 07-JUL-1999
LOCUS Human metabotropic glutamate receptor 4 mRNA, complete cds.

DEFINITION
U92457
U92457.1 GI:1935038

KEYWORDS
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 3431)
Wu, S. and Belagaje, R.M.
Direct Submission
Submitted (07-MAR-1997) mc625, Eli Lilly and Company, Lilly
Corporate Center, Indianapolis, IN 46285, USA
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ORIGIN

Query Match 83.8%; Score 1470.8; DB 9; Length 3431;
 Best Local Similarity 91.1%; Pred. No. 2e-233;
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QY 762 GTGGGACTCGCGTGGGCGCTGCTGCCCTCTTCTGCGCGCTGGTGGGATCGCGCCAC 821
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QY 1002 CATGAGCATCAGTACGCGGCGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTGA 1061
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QY 1062 CGAGGGCAAAACGCTCGGTGAGTGGCGCGCTTTCATCAGCCCGGCTCGACGCTGCCAT 1121
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QY 1182 CTCGCCACTCGGTGGTGGACTTCCAGGACCAACGAGACATTCGACCCCGCTTCCGAGGG 1241
 DB 2191 CTCGCCACTCGGTGGTGGACTTCCAGGACCAACGAGACATTCGACCCCGCTTCCGAGGG 2250

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QY 1422 CCCCATCTTTTGGACCTCACAGTCAGCGCAAGCTGTACATCCAGACCAACACACT 1481
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QY 1662 TGGGGAAGCCAAATCAGAGCTGTGTGAACCTTGGAGACCCCGAGCGCTGGCTTACCAACA 1721
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QY 1722 GACTACGTACCTACACCAACCATGCTCATAG 1755
 DB 2731 GACTACGTACCTACACCAACCATGCTCATAG 2764

RESULT 10
AKI22836

LOCUS
 DEFINITION Homo sapiens cDNA FLJ16445 fis, clone BRAMY308937, highly similar to Metabotropic glutamate receptor 4 precursor.

ACCESSION AKI22836

VERSION AKI22836.1 GI:34528033

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,

Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiraori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ieshibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hiraio,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsuura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togaishi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S. Complete sequencing and characterization of 21,243 full-length human cDNAs		
TITLE	Nat. Genet. 36 (1), 40-45 (2004)	
JOURNAL	14702039	
PUBMED	2	
REFERENCE	Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Muesashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.	
TITLE	NEDO human cDNA sequencing project	
JOURNAL	Unpublished	
REFERENCE	3 (bases 1 to 3850)	
AUTHORS	Isogai,T. and Yamamoto,J.	
TITLE	Direct Submission	
JOURNAL	Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team) ; 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)	
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) ; cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.	
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Best Local Similarity	91.1%; Pred. No. 1.9e-233;	
Matches 1562; Conservative	0; Mismatches 152; Indels 0; Gaps 0;	
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RESULT 11
A46196
LOCUS A46196 3884 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 3 from Patent WO9522609.
ACCESSION A46196
VERSION A46196.1 GI:2300444
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 3884)
AUTHORS Makoff,A.J.
TITLE HUMAN GLUTAMATE RECEPTOR PROTEINS
JOURNAL Patent: WO 9522609-A 3 24-AUG-1995;
WELLCOME FOUND (GB)
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ORIGIN
Query Match 83.8%; Score 1470.8; DB 6; Length 3884;
Best Local Similarity 91.1%; Pred. No. 1.9e-253;
Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
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DB 1376 GAGGGGAGGTGACGTTGCTGATTGAGCGCTGTGTACGCCATGGGCGACGCGCTGCACGC 1435
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DB 1976 GTTGTCTGCTGGTGTGACGTTTGTGCGCTACAAAGATACCCCGCATCGTCAAGGCTCGGG 2035
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Qy	1302	GCTGATGTGTCAGTGTATGTTGATCGGCATCAAGACCCGAGGCGTGGCCGAGACCTTCAA	1361
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Qy	1482	GACGCTCTCGGTGAGTCTGAGCGCTTCACTGCTGCTGCTGGGATGCTATACATGCCCAAGT	1541
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RESULT 12
AR270511
LOCUS AR270511 3884 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1074 from patent US 6500938.
ACCESSION AR270511
VERSION AR270511.1 GI:29701745
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3884)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression

JOURNAL FEATURES	Patent: US 6500938-A 1074 31-DEC-2002;		
source	1..3884		
ORIGIN	/organism="unknown"		
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Query Match	83.8%; Score 1470.8; DB 6; Length 3884;		
Best Local Similarity	91.1%; Pred. No. 1.9e-233;		
Matches 1562; Conservative	0; Mismatches 152; Indels 0; Gaps 0;		
Qy	42	AGGTTTCGACCGATATCTTCCAGCCGACGCTGGACAAACAGAGGCGCAACATCTGGTT	101
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Qy	222	GGAGGGAAGGTGCAGTTTCGTGATTGACGCTGTGTACGCCATGAGGCCACGCGCTGCAGC	281
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LOCUS AR381464

DEFINITION Sequence 14 from patent US 5608176.

ACCESSION AR381464

VERSION AR381464.1 GI:40089522

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3884)

AUTHORS Chaudhuri, N. and Roper, S.D.

TITLE Taste receptor for umami (monosodium glutamate) taste

JOURNAL Patent: US 5608176-A 14 19-AUG-2003;

FEATURES

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ORIGIN

Query Match 83.8%; Score 1470.8; DB 6; Length 3884;

Best Local Similarity 91.1%; Pred. No. 1.9e-233;

Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

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RESULT 14
AX548890
LOCUS
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Sequence 175 from Patent WO02061087.
ACCESSION
AX548890
VERSION
AX548890.1
KEYWORDS
GI:25813754
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Burner,G.C., Roush,C.L. and Brown,J.P.
TITLE
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL
Patent: WO 02061087-A 175 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN

Query Match 83.8%; Score 1470.8; DB 6; Length 3884;
Best Local Similarity 91.1%; Pred. No. 1.9e-233; Indels 0; Gaps 0;
Matches 1562; Conservative 0; Mismatches 152;
QY 42 AGGGTTGCACCGATCTTCTCAGCCGCACTCTGAGCAACAAAGGGGCAACATCTGGTT 101
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DEFINITION Sequence 83 from Patent WO03000928.
ACCESSION AX658167
VERSION AX658167.1 GI:29160742
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REFERENCE 1
AUTHORS Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,
Petersen,M.W. and Eisner,H.I.
TITLE Methods for identification of cancer cell surface molecules and
cancer specific promoters, and therapeutic uses thereof
JOURNAL Patent: WO 03000928-A 83 03-JAN-2003;
Odin Medical A/S (DK)
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ORIGIN
Query Match 83.8%; Score 1470.8; DB 6; Length 3884;
Best Local Similarity 91.1%; Pred. No. 1.9e-233;
Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
QY 42 AGGGTTCCAGCGATATTTCTCCAGCGCAGCTGTGGACAACAGCGCAACATCTGGTT 101
1196 AGGGTTCCAGCGCTACTTCTCCAGCGCAGCTGTGGACAACAGCGCAACATCTGGTT 1255
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